


```
Db 541 GGATNGNTNGAANGAANGAANCAAAAAAGTNNANAAATGGNGTAAAGTNNNTT 600
QY 601 nntnnnaaaganganttcnaatntnngntcaatnatacgangabacnngancnaa 660
    |||
Db 601 nntnnnnnaaganganttcnaatntnngntcaatnatacgangabacnngancnaa 660
QY 661 ngnttunnngatnngangannttntantanaangntnnnnnatctnnaaagan 720
    |||
Db 661 NGNTTNNNGATNGANGAANNNTTNTANTANAANGNTNNNNNATTTNNAAGANN 720
QY 721 ngntnngtncnntngcnaatnataatctgatactnntnnngaanntnannnga 780
    |||
Db 721 NGTNTNGTNCNTNGCNAATATNNANTTGTAGANTNTNNNNGAANTNNANNNGA 780
QY 781 nngnnnnnnntnaataaagannnaaagcnnntnaangantnganaaangccnga 840
    |||
Db 781 NNGNNNNNNNTNAATAAGANNNAANAAGCNTNNAAGANTNGANAANAAGCCNGA 840
QY 841 naaaaaaangcnnnaaannnnnnnaannntnaaanaaantnnngcnaannca 900
    |||
Db 841 NAAANAAAAANGCNNNAANAANNNNNNNAANTNNAANANCAANTNNNGCAANNANCA 900
QY 901 aaantnnanganannnnnnntnaannnnncaatgnaangaatccnntcngc 960
    |||
Db 901 AAANTNNANGANNANNNNNNNTNNAANNNNANCATGGAANGAATTACCNATNTCNGC 960
QY 961 ngntnctntnatnaatcctnltgaagtngtntantngcngtgnacnctnaatn 1020
    |||
Db 961 NGNTNCTTNTNATNAATCCNTNTGAAGTNGTNTANTANGCNGGTGACNTCAATNN 1020
QY 1021 nctnnngcancntngcngnagntatgcnntncaatgcnngnatgataatgcnntna 1080
    |||
Db 1021 NTNNNGCANTNGCNGNAGNTATGCTNTNCAATGCGNNNATGATTAAATATGCNNTNNA 1080
QY 1081 ncatnnatcnaangntanaatctntatgnttgaagnttgaagnttannngangcnga 1140
    |||
Db 1081 NCATNNNATNNNANGNTANAATTTNTATGCGNTTGAAGNTTANTANGANGCNGA 1140
QY 1141 agatnngngntnntaanttnaaaaangntnnnatgcnngantntnngantngtgg 1200
    |||
Db 1141 AGATGNGGNGTNTNTAAATTTNAAAAANGNTNNNATGCGNANTNTNGANTANGTTGG 1200
QY 1201 ngantntnaaacnataaanaancnntntannnnnnntatannncantnaaaaaant 1260
    |||
Db 1201 NGANTTNTNTAAACCATATAAANAANCNTNTANNNNNNNTATANNNCANTNAAAAANT 1260
QY 1261 naannnaannnnnnntaannnaannnnnnnaannnnnnnnnatgaaattacaga 1320
    |||
Db 1261 NNAANNNNANNNNNNTTANNNAANNNNNNNANNNNNNNNNAATGAATTACAGA 1320
QY 1321 gttaaann 1328
    |||
Db 1321 GTTAAANN 1328
```

Search completed: June 22, 2002, 09:59:34
Job time: 7482 sec

Db 241 ncnngtnatngattnananaannnagancngtngtncantntctttaanganttnmmaa 300
QY 301 ntactnaaanaannannntnnntatannntnnntngancntannntnctatcaata 360
Db 301 ntactnaaanaannannntnnntatannntnnntngancntannntnctatcaata 360
QY 361 nnnaatcatgagnganttnnnngnaatcgngngnanga ttggnnttngatnann 420
Db 361 nnnaatcatgagnganttnnnngnaatcgngngnanga ttggnnttngatnann 420
QY 421 nnnnnnnntngnttnaanaannngnttnnnannngnttgancntnnnccaat 480
Db 421 nnnnnnnntngnttnaanaannngnttnnnannngnttgancntnnnccaat 480
QY 481 nngntncaatcngnttnattnannnnnaaaannncnnaanganttnnaannnat 540
Db 481 nngntncaatcngnttnattnannnnnaaaannncnnaanganttnnaannnat 540
QY 541 gga tngntngnaaanngnanaaanaaaagttnanaanaa tggngtnaaagtannnt 600
Db 541 gga tngntngnaaanngnanaaanaaaagttnanaanaa tggngtnaaagtannnt 600
QY 601 nntnnnnnaaagangantncnaatnttngntcattnatgagngatcacnnganncnaa 660
Db 601 nntnnnnnaaagangantncnaatnttngntcattnatgagngatcacnnganncnaa 660
QY 661 ngnntnnnnngatngngannnnnttnatanaaannngtnnnnnnattnnaaagann 720
Db 661 ngnntnnnnngatngngannnnnttnatanaaannngtnnnnnnattnnaaagann 720
QY 721 ngtntngtncnntngcntata tnnantttgatgntannntnnnnga 780
Db 721 ngtntngtncnntngcntata tnnantttgatgntannntnnnnga 780
QY 781 nngnannnnntnaatcaaaagannnaanaaagcmtnaaangantnanaaangncnga 840
Db 781 nngnannnnntnaatcaaaagannnaanaaagcmtnaaangantnanaaangncnga 840
QY 841 naaanaaaangcnnnaanaaannnnnnnaaanttnaanaanaaannngcnaaannaca 900
Db 841 naaanaaaangcnnnaanaaannnnnnnaaanttnaanaanaaannngcnaaannaca 900
QY 901 aaaaantnangagngannnnnnnttnaannnancatggnaaagaattacna tntcngc 960
Db 901 aaaaantnangagngannnnnnnttnaannnancatggnaaagaattacna tntcngc 960
QY 961 ngnntccttnatnaatcctntgaagtngtntan tangucngtgcnaatcnaatn 1020
Db 961 ngnntccttnatnaatcctntgaagtngtntan tangucngtgcnaatcnaatn 1020
QY 1021 nttnngcacttngcngnagatcgtcmtncatggnnatgtaantatgcnhtna 1080
Db 1021 nttnngcacttngcngnagatcgtcmtncatggnnatgtaantatgcnhtna 1080
QY 1081 ncattnnattnanngntanaaatttnatggnnttaagngttnantttanngangangcga 1140
Db 1081 ncattnnattnanngntanaaatttnatggnnttaagngttnantttanngangangcga 1140
QY 1141 agatgngnggnttnaanttnaanaaangntnnnatgcnangantntngantngtgg 1200
Db 1141 agatgngnggnttnaanttnaanaaangntnnnatgcnangantntngantngtgg 1200
QY 1201 nganttnatnaaaccnatanaaancnnttnannnnntatannncantnaaaannt 1260
Db 1201 nganttnatnaaaccnatanaaancnnttnannnnntatannncantnaaaannt 1260
QY 1261 nnaannnaannnnnnntannnaannnnnnnaannnaannnnnnatgaaattacaga 1320
Db 1261 nnaannnaannnnnnntannnaannnnnnnaannnaannnnnnatgaaattacaga 1320
QY 1321 gtttaann 1328
Db 1321 gtttaann 1328

Search completed: June 22, 2002, 10:04:59
Job time: 7532 sec

us-09-509-234c-1.oligo50.rni

Wed Jun 26 08:06:16 2002

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 22, 2002, 07:55:47 ; Search time 53.69 Seconds
(without alignments)
6075.643 Million cell updates/sec

Title: US-09-509-234C-1
Perfect score: 1328
Sequence: 1 nnnnnnnnnnnnaatga.....gaaatttacagagttaannn 1328

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 383533 seqs, 122816752 residues

Word size : 50

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description

No matches found

Search completed: June 22, 2002, 10:00:41
Job time: 7494 sec

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OM nucleic - nucleic search, using sw model

Run on: June 22, 2002, 07:51:27 ; Search time 1732.3 Seconds
(without alignments)
10346.912 Million cell updates/sec

Title: US-09-509-234C-1
Perfect score: 1328
Sequence: 1 nnnnnnnnnnnanaatga.....gaaattacagagttaannn 1328

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 13736207 seqs, 6748477542 residues

Word size : 50

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : EST:*

1:	em_estba:*
2:	em_esthum:*
3:	em_estin:*
4:	em_estnu:*
5:	em_estov:*
6:	em_estpl:*
7:	em_estro:*
8:	em_htc:*
9:	gb_est1:*
10:	gb_est2:*
11:	gb_htc:*
12:	gb_gss:*
13:	em_gss_hum:*
14:	em_gss_inv:*
15:	em_gss_pln:*
16:	em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result	Query		
No.	Score	Match Length DB ID	Description

No matches found

Search completed: June 22, 2002, 09:17:10
Job time: 5143 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 22, 2002, 05:48:26 ; Search time 2531.75 Seconds
(without alignments)
10976.771 Million cell updates/sec

Title: US-09-509-234C-1

Perfect score: 1328

Sequence: 1 nnnnnnnnnnnnaatga.....gaattacagagtttaannn 1328

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1797656 seqs, 10463268293 residues

Word size : 15

Total number of hits satisfying chosen parameters: 10912

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

GenEmbl:*

1: gb_ba:*

2: gb_htg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vi:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_om:*

21: em_or:*

22: em_ov:*

23: em_pat:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_sts:*

28: em_un:*

29: em_vi:*

30: em_htg_hum:*

31: em_htg_inv:*

32: em_htg_other:*

33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query - Score	Match Length	ID	Description
------------	---------------	--------------	----	-------------

1	1328	100.0	1328	6	A97445
2	44	3.3	44	6	A97468
3	43	3.2	43	6	A97454
4	40	3.0	40	6	A97457
5	37	2.8	37	6	A97451
6	35	2.6	35	6	A97446
7	35	2.6	35	6	A97452
8	35	2.6	35	6	A97467
9	32	2.4	32	6	A97459
10	32	2.4	32	6	A97466
11	25	1.9	25	6	A97449
12	25	1.9	13139	2	AC107183
13	25	1.9	59240	2	AC108260
14	25	1.9	124083	2	AC109815
15	24	1.8	50132	2	AC098325
16	24	1.8	55797	2	AC110037
17	24	1.8	58555	2	AC102082
18	24	1.8	60536	2	AC102614
19	24	1.8	61916	2	AC097985
20	24	1.8	62897	2	AC101230
21	24	1.8	67602	2	AC101929
22	24	1.8	68380	2	AC102929
23	24	1.8	68896	2	AC101013
24	24	1.8	73483	2	AC097933
25	24	1.8	73745	2	AC044897
26	24	1.8	75609	2	AC094802
27	24	1.8	75839	2	AC037462
28	24	1.8	105364	2	AC097948
29	24	1.8	115905	2	AC096477
30	24	1.8	120441	2	AC098872
31	24	1.8	134260	2	AC094356
32	24	1.8	141892	2	AC023197
33	24	1.8	147138	2	AC095329
34	24	1.8	151452	2	AC097979
35	24	1.8	160791	2	AC094557
36	24	1.8	164988	2	AC094890
37	24	1.8	170330	2	AC106291
38	24	1.8	173793	2	AC096176
39	24	1.8	175229	2	AC096209
40	24	1.8	178214	2	AC096965
41	24	1.8	180248	2	AC096191
42	24	1.8	182686	2	AC098098
43	24	1.8	298166	2	AC087563
44	23	1.7	737	6	AR008392
45	23	1.7	737	6	I87384
46	23	1.7	66624	2	AC04376
47	23	1.7	69274	2	AC084228
48	23	1.7	77772	2	AC027549
49	23	1.7	119492	2	AC096479
50	23	1.7	121290	2	CEH27C14
51	23	1.7	131145	2	AC108525
52	23	1.7	182948	2	AC098130
53	22	1.7	22	6	A97464
54	22	1.7	127	9	HS22QT015
55	22	1.7	52668	2	AC102838
56	22	1.7	59257	2	AC103686
57	22	1.7	77137	2	AC097748
58	22	1.7	88989	2	AC096476
59	22	1.7	156785	2	AC103440
60	22	1.7	164039	2	AC099084
61	22	1.7	173835	2	AC096011
62	22	1.7	194846	2	AC095597
63	21	1.6	51870	2	AC107965
64	21	1.6	52390	2	AC100498
65	21	1.6	52611	2	AC100025
66	21	1.6	57550	2	AC100408
67	21	1.6	58445	2	AC101264
68	21	1.6	61352	2	AC099964
69	21	1.6	67568	2	AC105907
70	21	1.6	68108	2	AC090474
71	21	1.6	74306	2	AC022623
72	21	1.6	86026	2	AC106588
73	21	1.6	110000	2	AC099646_0

C 74	21	1.6	149098	2	AC098108	AC098108 Rattus no	C 147	19	1.4	59886	2	AC083766	AC083766 Homo sapi
C 75	21	1.6	151452	2	AC097979	AC097979 Rattus no	C 148	19	1.4	60130	2	AC105157	AC105157 Mus muscu
C 76	21	1.6	157871	2	AC025074	AC025074 Homo sapi	C 149	19	1.4	60343	2	AC099872	AC099872 Mus muscu
C 77	21	1.6	181705	2	AC023831	AC023831 Homo sapi	C 150	19	1.4	60422	2	AC087584	AC087584 Homo sapi
C 78	21	1.6	183624	2	AL512588	AL512588 Mus muscu	C 151	19	1.4	60504	2	AC090716	AC090716 Homo sapi
C 79	21	1.6	185565	2	AC020607	AC020607 Homo sapi	C 152	19	1.4	61240	2	AC068578	AC068578 Homo sapi
C 80	21	1.6	211967	2	AC013368	AC013368 Homo sapi	C 153	19	1.4	62166	2	AC107676	AC107676 Mus muscu
C 81	20	1.5	20	6	A97458	A97458 Sequence 14	C 154	19	1.4	62795	2	AC022602	AC022602 Homo sapi
C 82	20	1.5	20	6	A97470	A97470 Sequence 26	C 155	19	1.4	63205	2	AC091186	AC091186 Homo sapi
C 83	20	1.5	43057	2	AC016312	AC016312 Homo sapi	C 156	19	1.4	63515	2	AC101883	AC101883 Mus muscu
C 84	20	1.5	43057	2	AC100775	AC100775 Homo sapi	C 157	19	1.4	63573	2	AC108390	AC108390 Mus muscu
C 85	20	1.5	5069	2	AC018631	AC018631 Drosophila	C 158	19	1.4	64742	2	AC110518	AC110518 Mus muscu
C 86	20	1.5	58572	2	AC090935	AC090935 Homo sapi	C 159	19	1.4	65144	2	AC109169	AC109169 Mus muscu
C 87	20	1.5	59058	2	AC108444	AC108444 Mus muscu	C 160	19	1.4	65265	2	AC101737	AC101737 Mus muscu
C 88	20	1.5	59909	2	AC090996	AC090996 Homo sapi	C 161	19	1.4	65940	2	AC103716	AC103716 Homo sapi
C 89	20	1.5	63059	2	AC101498	AC101498 Homo sapi	C 162	19	1.4	68323	2	AC102528	AC102528 Mus muscu
C 90	20	1.5	64360	2	AC104343	AC104343 Homo sapi	C 163	19	1.4	69368	2	AC101500	AC101500 Mus muscu
C 91	20	1.5	66240	2	AC090633	AC090633 Homo sapi	C 164	19	1.4	69664	2	AC022737	AC022737 Homo sapi
C 92	20	1.5	67499	2	AC101967	AC101967 Mus muscu	C 165	19	1.4	70308	2	AC073899	AC073899 Homo sapi
C 93	20	1.5	67963	2	AC108411	AC108411 Homo sapi	C 166	19	1.4	70433	2	AC102325	AC102325 Mus muscu
C 94	20	1.5	69156	2	AC087291	AC087291 Homo sapi	C 167	19	1.4	71792	2	AC102402	AC102402 Mus muscu
C 95	20	1.5	69961	2	AC102179	AC102179 Mus muscu	C 168	19	1.4	71820	2	AC100627	AC100627 Mus muscu
C 96	20	1.5	71226	2	AC101601	AC101601 Mus muscu	C 169	19	1.4	72192	2	AC101657	AC101657 Homo sapi
C 97	20	1.5	71833	2	AC102178	AC102178 Mus muscu	C 170	19	1.4	74101	2	AC087751	AC087751 Homo sapi
C 98	20	1.5	74412	2	AC020767	AC020767 Homo sapi	C 171	19	1.4	76856	2	AC021526	AC021526 Homo sapi
C 99	20	1.5	76900	2	AC060787	AC060787 Homo sapi	C 172	19	1.4	79795	2	AC015790	AC015790 Homo sapi
C 100	20	1.5	102069	2	AC095721	AC095721 Rattus no	C 173	19	1.4	82939	2	AC106210	AC106210 Rattus no
C 101	20	1.5	149864	2	AC098060	AC098060 Rattus no	C 174	19	1.4	85722	2	AC094640	AC094640 Homo sapi
C 102	20	1.5	150845	2	AC095328	AC095328 Rattus no	C 175	19	1.4	91334	2	AC024691	AC024691 Homo sapi
C 103	20	1.5	160048	2	AC105541	AC105541 Rattus no	C 176	19	1.4	99653	2	AC103038	AC103038 Rattus no
C 104	20	1.5	160086	2	AC098040	AC098040 Rattus no	C 177	19	1.4	110000	2	CEY39B6.0	CEY39B6.0
C 105	20	1.5	168576	2	AL512584	AL512584 Mus muscu	C 178	19	1.4	112259	2	AC091087	AC091087 Homo sapi
C 106	20	1.5	169323	2	AL161906	AL161906 Homo sapi	C 179	19	1.4	124182	2	AC091087	AC091087 Homo sapi
C 107	20	1.5	169389	2	AC025243	AC025243 Homo sapi	C 180	19	1.4	126038	2	AC094335	AC094335 Rattus no
C 108	20	1.5	172080	2	AC025677	AC025677 Homo sapi	C 181	19	1.4	126938	2	AC094335	AC094335 Rattus no
C 109	20	1.5	183624	2	AC020554	AC020554 Homo sapi	C 182	19	1.4	127505	2	AC061980	AC061980 Homo sapi
C 110	20	1.5	188751	2	AC094179	AC094179 Rattus no	C 183	19	1.4	131271	2	AC015927	AC015927 Homo sapi
C 111	20	1.5	191692	2	AC023834	AC023834 Mus muscu	C 184	19	1.4	134323	2	AC106298	AC106298 Rattus no
C 112	20	1.5	229482	2	AC074149	AC074149 Mus muscu	C 185	19	1.4	134507	2	AC103158	AC103158 Homo sapi
C 113	20	1.5	234407	2	AL670999	AL670999 Mus muscu	C 186	19	1.4	135095	2	AC084714	AC084714 Homo sapi
C 114	20	1.5	267759	2	AC079418	AC079418 Mus muscu	C 187	19	1.4	135350	2	AL391626	AL391626 Rattus no
C 115	20	1.5	274626	2	AC006903	AC006903 Caenorhabd	C 188	19	1.4	135671	2	AC107529	AC107529 Homo sapi
C 116	19	1.4	641	6	A97472	A97472 Sequence 28	C 189	19	1.4	136817	2	AC022476	AC022476 Homo sapi
C 117	19	1.4	641	6	HS437181	AJ37181 Homo sapi	C 190	19	1.4	140910	2	AC104095	AC104095 Homo sapi
C 118	19	1.4	724	11	AJ046676	AJ046676 Rattus no	C 191	19	1.4	143509	2	AC068683	AC068683 Homo sapi
C 119	19	1.4	874	6	HS3324047	AJ24047 Homo sapi	C 192	19	1.4	146348	2	AC103436	AC103436 Homo sapi
C 120	19	1.4	1254	6	AJ141473	AJ141473 Sequence	C 193	19	1.4	146473	2	AC013344	AC013344 Homo sapi
C 121	19	1.4	1260	6	SH023712	U23712 Staphylococ	C 194	19	1.4	147839	2	AC106427	AC106427 Rattus no
C 122	19	1.4	1283	6	A97490	A97490 Sequence 46	C 195	19	1.4	148524	2	AC098145	AC098145 Homo sapi
C 123	19	1.4	1284	6	A97494	A97494 Sequence 50	C 196	19	1.4	150083	2	AC024892	AC024892 Homo sapi
C 124	19	1.4	1295	6	A97488	A97488 Sequence 44	C 197	19	1.4	153938	2	AC080050	AC080050 Homo sapi
C 125	19	1.4	1297	6	A97492	A97492 Sequence 48	C 198	19	1.4	154289	2	AC098114	AC098114 Rattus no
C 126	19	1.4	1305	6	A97484	A97484 Sequence 40	C 199	19	1.4	155825	2	AC106084	AC106084 Rattus no
C 127	19	1.4	1327	6	SE023714	U23714 Staphylococ	C 200	19	1.4	156062	2	AC097255	AC097255 Rattus no
C 128	19	1.4	1377	1	SE023713	U23713 Staphylococ	C 201	19	1.4	163134	2	AC019286	AC019286 Homo sapi
C 129	19	1.4	1877	1	SAFEA	X17688 S.aureus fa	C 202	19	1.4	168836	2	AC105590	AC105590 Homo sapi
C 130	19	1.4	4434	6	AF269697	AF269697 Staphyloc	C 203	19	1.4	168836	2	AC105590	AC105590 Homo sapi
C 131	19	1.4	4434	6	AF269697	AF269697 Staphyloc	C 204	19	1.4	168836	2	AC105590	AC105590 Homo sapi
C 132	19	1.4	4434	6	AF269697	AF269697 Staphyloc	C 205	19	1.4	168836	2	AC105590	AC105590 Homo sapi
C 133	19	1.4	14118	2	AC109833	AC109833 Rattus no	C 206	19	1.4	170981	2	AC097596	AC097596 Homo sapi
C 134	19	1.4	23864	3	AE002853	AE002853 Drosophila	C 207	19	1.4	170993	2	AC021528	AC021528 Homo sapi
C 135	19	1.4	34865	3	AC098363	AC098363 Rattus no	C 208	19	1.4	171233	2	AC106449	AC106449 Rattus no
C 136	19	1.4	38639	2	AC103279	AC103279 Rattus no	C 209	19	1.4	171965	2	AC027507	AC027507 Homo sapi
C 137	19	1.4	40080	2	AC011563	AC011563 Homo sapi	C 210	19	1.4	175108	2	AC031982	AC031982 Homo sapi
C 138	19	1.4	46200	2	AC100254	AC100254 Mus muscu	C 211	19	1.4	177671	2	AC106096	AC106096 Homo sapi
C 139	19	1.4	46200	2	AC108660	AC108660 Rattus no	C 212	19	1.4	178535	2	AC055755	AC055755 Homo sapi
C 140	19	1.4	49530	2	AC102361	AC102361 Mus muscu	C 213	19	1.4	180207	2	AC060802	AC060802 Homo sapi
C 141	19	1.4	51163	2	AC067930	AC067930 Homo sapi	C 214	19	1.4	180341	2	AC094468	AC094468 Homo sapi
C 142	19	1.4	55205	2	AC102492	AC102492 Mus muscu	C 215	19	1.4	180918	2	AC106543	AC106543 Rattus no
C 143	19	1.4	56191	2	AC103162	AC103162 Rattus no	C 216	19	1.4	184535	2	CNS057CJ	CNS057CJ Homo sapi
C 144	19	1.4	56494	2	AC083782	AC083782 Homo sapi	C 217	19	1.4	193581	2	PFMAL13P1	PFMAL13P1 Plasmodu
C 145	19	1.4	57573	2	AC087509	AC087509 Homo sapi	C 218	19	1.4	201470	2	AC073924	AC073924 Homo sapi
C 146	19	1.4	58737	2	AC109338	AC109338 Homo sapi	C 219	19	1.4	202777	2	AL590380	AL590380 Mus muscu

c 220	19	1.4	202777	2	AL590380	Mus muscu	AL590380 Mus muscu	18	1.4	5556	2	AC100220	Mus muscu	AC100220 Mus muscu
c 221	19	1.4	207101	2	AL663092	Mus muscu	AL663092 Mus muscu	18	1.4	5563	2	AC103997	Homo sapi	AC103997 Homo sapi
c 222	19	1.4	207962	2	AC015679	Homo sapi	AC015679 Homo sapi	18	1.4	5568	2	AC102000	Mus muscu	AC102000 Mus muscu
c 223	19	1.4	209112	2	AC104468	Homo sapi	AC104468 Homo sapi	18	1.4	56010	2	AC102406	Mus muscu	AC102406 Mus muscu
c 224	19	1.4	221377	2	AL662813	Mus muscu	AL662813 Mus muscu	18	1.4	56010	2	AC102406	Mus muscu	AC102406 Mus muscu
c 225	19	1.4	303750	1	AP003133	Staphyloc	AP003133 Staphyloc	18	1.4	56330	2	AC101316	Mus muscu	AC101316 Mus muscu
c 226	19	1.4	303750	1	AP003133	Staphyloc	AP003133 Staphyloc	18	1.4	56330	2	AC101316	Mus muscu	AC101316 Mus muscu
c 227	19	1.4	328117	2	AC017097	Homo sapi	AC017097 Homo sapi	18	1.4	56342	2	AC101808	Rattus no	AC101808 Rattus no
c 228	19	1.4	346900	1	AP003362	Staphyloc	AP003362 Staphyloc	18	1.4	56565	2	AC106398	Rattus no	AC106398 Rattus no
c 229	18	1.4	18	6	A97453	Sequence 9	A97453 Sequence 9	18	1.4	56609	2	AC102570	Mus muscu	AC102570 Mus muscu
c 230	18	1.4	200	11	G37938	G37938 c4M72 Plasm	G37938 c4M72 Plasm	18	1.4	56751	2	AC100850	Homo sapi	AC100850 Homo sapi
c 231	18	1.4	1023	6	A65498	Sequence 11	A65498 Sequence 11	18	1.4	56779	2	AC106980	Rattus no	AC106980 Rattus no
c 232	18	1.4	1371	6	A97497	Sequence 53	A97497 Sequence 53	18	1.4	56793	2	AC101622	Mus muscu	AC101622 Mus muscu
c 233	18	1.4	10606	2	AC109663	Rattus no	AC109663 Rattus no	18	1.4	57398	2	AC027586	Homo sapi	AC027586 Homo sapi
c 234	18	1.4	10876	2	AC108448	Homo sapi	AC108448 Homo sapi	18	1.4	57417	2	AC102235	Mus muscu	AC102235 Mus muscu
c 235	18	1.4	24314	2	AC110387	Homo sapi	AC110387 Homo sapi	18	1.4	57550	2	AC069034	Homo sapi	AC069034 Homo sapi
c 236	18	1.4	24412	2	AC100285	Rattus no	AC100285 Rattus no	18	1.4	57684	2	AC108066	Homo sapi	AC108066 Homo sapi
c 237	18	1.4	27439	2	AC1007843	Mus muscu	AC1007843 Mus muscu	18	1.4	57866	2	AC102789	Mus muscu	AC102789 Mus muscu
c 238	18	1.4	31191	2	AC108328	Rattus no	AC108328 Rattus no	18	1.4	58272	2	AC090171	Homo sapi	AC090171 Homo sapi
c 239	18	1.4	39799	2	AC074056	Homo sapi	AC074056 Homo sapi	18	1.4	58401	2	AC102744	Mus muscu	AC102744 Mus muscu
c 240	18	1.4	40911	2	AC101783	Mus muscu	AC101783 Mus muscu	18	1.4	59648	2	AC099825	Papio ham	AC099825 Papio ham
c 241	18	1.4	42611	2	AC100090	Mus muscu	AC100090 Mus muscu	18	1.4	59937	2	AC069566	Homo sapi	AC069566 Homo sapi
c 242	18	1.4	43159	2	AC102354	Mus muscu	AC102354 Mus muscu	18	1.4	70105	2	AC102180	Mus muscu	AC102180 Mus muscu
c 243	18	1.4	43918	2	AC108595	Rattus no	AC108595 Rattus no	18	1.4	70534	2	AC101820	Mus muscu	AC101820 Mus muscu
c 244	18	1.4	45408	2	AC087406	Homo sapi	AC087406 Homo sapi	18	1.4	70816	2	AC101610	Mus muscu	AC101610 Mus muscu
c 245	18	1.4	45908	2	AC105240	Homo sapi	AC105240 Homo sapi	18	1.4	70830	2	AC103367	Mus muscu	AC103367 Mus muscu
c 246	18	1.4	46377	2	AC024365	Homo sapi	AC024365 Homo sapi	18	1.4	70830	2	AC103367	Mus muscu	AC103367 Mus muscu
c 247	18	1.4	47123	2	AC100792	Homo sapi	AC100792 Homo sapi	18	1.4	71139	2	AC102101	Mus muscu	AC102101 Mus muscu
c 248	18	1.4	47885	2	AC099926	Mus muscu	AC099926 Mus muscu	18	1.4	71363	2	AC104346	Homo sapi	AC104346 Homo sapi
c 249	18	1.4	51658	2	AC109063	Rattus no	AC109063 Rattus no	18	1.4	71465	2	AC101119	Mus muscu	AC101119 Mus muscu
c 250	18	1.4	51681	2	AC101239	Mus muscu	AC101239 Mus muscu	18	1.4	71858	2	AC101318	Homo sapi	AC101318 Homo sapi
c 251	18	1.4	51832	2	AC101875	Homo sapi	AC101875 Homo sapi	18	1.4	71876	2	AP000631	Mus muscu	AP000631 Mus muscu
c 252	18	1.4	52082	2	AC103712	Mus muscu	AC103712 Mus muscu	18	1.4	72016	2	AC026574	Homo sapi	AC026574 Homo sapi
c 253	18	1.4	53579	2	AC091642	Mus muscu	AC091642 Mus muscu	18	1.4	72299	2	AC101990	Mus muscu	AC101990 Mus muscu
c 254	18	1.4	53823	2	AC091642	Mus muscu	AC091642 Mus muscu	18	1.4	72648	2	AC101171	Mus muscu	AC101171 Mus muscu
c 255	18	1.4	54501	2	AC102416	Mus muscu	AC102416 Mus muscu	18	1.4	73193	2	AC102579	Mus muscu	AC102579 Mus muscu
c 256	18	1.4	5629	2	AC109287	Mus muscu	AC109287 Mus muscu	18	1.4	73402	2	AC101535	Mus muscu	AC101535 Mus muscu
c 257	18	1.4	56609	2	AC101764	Mus muscu	AC101764 Mus muscu	18	1.4	73402	2	AC101535	Mus muscu	AC101535 Mus muscu
c 258	18	1.4	56822	2	AC091084	Homo sapi	AC091084 Homo sapi	18	1.4	75020	2	AC091041	Mus muscu	AC091041 Mus muscu
c 259	18	1.4	57591	2	AC069490	Homo sapi	AC069490 Homo sapi	18	1.4	76318	2	AC106419	Rattus no	AC106419 Rattus no
c 260	18	1.4	57714	2	AC107999	Homo sapi	AC107999 Homo sapi	18	1.4	77467	2	AC025101	Homo sapi	AC025101 Homo sapi
c 261	18	1.4	58067	2	AC100426	Mus muscu	AC100426 Mus muscu	18	1.4	77836	2	AC022573	Homo sapi	AC022573 Homo sapi
c 262	18	1.4	58183	2	AC105972	Mus muscu	AC105972 Mus muscu	18	1.4	78156	2	AC024976	Homo sapi	AC024976 Homo sapi
c 263	18	1.4	58445	2	AC084704	Mus muscu	AC084704 Mus muscu	18	1.4	79048	2	AC024976	Homo sapi	AC024976 Homo sapi
c 264	18	1.4	58827	2	AC103756	Homo sapi	AC103756 Homo sapi	18	1.4	79796	2	AC087326	Trypanoso	AC087326 Trypanoso
c 265	18	1.4	59165	2	AC091456	Mus muscu	AC091456 Mus muscu	18	1.4	80633	2	AC027503	Homo sapi	AC027503 Homo sapi
c 266	18	1.4	59903	2	AC015782	Mus muscu	AC015782 Mus muscu	18	1.4	81169	2	AC026595	Homo sapi	AC026595 Homo sapi
c 267	18	1.4	60726	2	AC100613	Mus muscu	AC100613 Mus muscu	18	1.4	83379	2	AC026595	Homo sapi	AC026595 Homo sapi
c 268	18	1.4	60867	2	AC110233	Mus muscu	AC110233 Mus muscu	18	1.4	87525	2	DMBR41A22	Drosophil	AL133496 Drosophil
c 269	18	1.4	61275	2	AC102012	Mus muscu	AC102012 Mus muscu	18	1.4	88382	2	AC018394	Homo sapi	AC018394 Homo sapi
c 270	18	1.4	62185	2	AC102565	Mus muscu	AC102565 Mus muscu	18	1.4	89388	2	AC096122	Rattus no	AC096122 Rattus no
c 271	18	1.4	62224	2	AC103862	Homo sapi	AC103862 Homo sapi	18	1.4	90108	2	AC021611	Homo sapi	AC021611 Homo sapi
c 272	18	1.4	62248	2	AC101017	Mus muscu	AC101017 Mus muscu	18	1.4	92535	2	AC093410	Oryctolag	AC093410 Oryctolag
c 273	18	1.4	62529	2	AC102074	Mus muscu	AC102074 Mus muscu	18	1.4	92677	2	AC009382	Drosophil	AC009382 Drosophil
c 274	18	1.4	62707	2	AC091197	Homo sapi	AC091197 Homo sapi	18	1.4	95242	2	AC105874	Rattus no	AC105874 Rattus no
c 275	18	1.4	62736	2	AC102774	Mus muscu	AC102774 Mus muscu	18	1.4	98229	2	AC106651	Rattus no	AC106651 Rattus no
c 276	18	1.4	63345	2	AC102648	Mus muscu	AC102648 Mus muscu	18	1.4	99482	2	AC096229	Rattus no	AC096229 Rattus no
c 277	18	1.4	63365	2	AC087437	Mus muscu	AC087437 Mus muscu	18	1.4	101391	2	AC098918	Rattus no	AC098918 Rattus no
c 278	18	1.4	63746	2	AC107680	Mus muscu	AC107680 Mus muscu	18	1.4	102317	2	AC106447	Rattus no	AC106447 Rattus no
c 279	18	1.4	63944	2	AC024955	Homo sapi	AC024955 Homo sapi	18	1.4	102835	2	AC091350	Rattus no	AC091350 Rattus no
c 280	18	1.4	64067	2	AC103962	Mus muscu	AC103962 Mus muscu	18	1.4	103182	2	AC105835	Rattus no	AC105835 Rattus no
c 281	18	1.4	64162	2	AC102104	Mus muscu	AC102104 Mus muscu	18	1.4	108155	2	AC105594	Rattus no	AC105594 Rattus no
c 282	18	1.4	64272	2	AC101276	Mus muscu	AC101276 Mus muscu	18	1.4	108271	2	AC105506	Rattus no	AC105506 Rattus no
c 283	18	1.4	64378	2	AC100024	Mus muscu	AC100024 Mus muscu	18	1.4	110000	2	AC015850	Homo sapi	AC015850 Homo sapi
c 284	18	1.4	64626	2	AC011641	Homo sapi	AC011641 Homo sapi	18	1.4	113553	2	AC106265	Rattus no	AC106265 Rattus no
c 285	18	1.4	64626	2	AC025070	Homo sapi	AC025070 Homo sapi	18	1.4	113679	2	AC096131	Mus muscu	AC096131 Mus muscu
c 286	18	1.4	64701	2	AC102892	Mus muscu	AC102892 Mus muscu	18	1.4	114149	2	AC099943	Mus muscu	AC099943 Mus muscu
c 287	18	1.4	64727	2	AC105065	Mus muscu	AC105065 Mus muscu	18	1.4	114243	2	AC096937	Rattus no	AC096937 Rattus no
c 288	18	1.4	64998	2	AC100780	Mus muscu	AC100780 Mus muscu	18	1.4	116508	2	AC011056	Homo sapi	AC011056 Homo sapi
c 289	18	1.4	65273	2	AC102550	Mus muscu	AC102550 Mus muscu	18	1.4	119909	2	AC068935	Homo sapi	AC068935 Homo sapi
c 290	18	1.4	65340	2	AC087759	Homo sapi	AC087759 Homo sapi	18	1.4	120902	2	AC107492	Rattus no	AC107492 Rattus no
c 291	18	1.4	65391	2	AC103333	Mus muscu	AC103333 Mus muscu	18	1.4	127044	2	AC106180	Rattus no	AC106180 Rattus no
c 292	18	1.4	65450	2	AC103333	Mus muscu	AC103333 Mus muscu	18	1.4	130583	2	AC007420	Drosophil	AC007420 Drosophil
								18	1.4	131594	2	DMBR17J10	Homo sapi	AL122026 Drosophil
								18	1.4	131967	2	AC016288	Homo sapi	AC016288 Homo sapi
								18	1.4	134172	2	AC098096	Rattus no	AC098096 Rattus no

C 366	18	1.4 134172	2	AC098096	Rattus no	C 439	18	1.4 185440	2	AC015499	AC015499 Homo sapi
C 367	18	1.4 137794	2	AC016854	Homo sapi	C 440	18	1.4 186706	2	AC068019	AC068019 Homo sapi
C 368	18	1.4 138857	2	AC027616	Homo sapi	C 441	18	1.4 188152	2	AC025847	AC025847 Homo sapi
C 369	18	1.4 141917	2	AL645926	Danio rer	C 442	18	1.4 189803	2	AC012542	AC012542 Homo sapi
C 370	18	1.4 142658	2	AC011135	Homo sapi	C 443	18	1.4 192060	2	AC106728	AC106728 Homo sapi
C 371	18	1.4 143585	2	AC013349	Homo sapi	C 444	18	1.4 192400	2	AC022712	AC022712 Homo sapi
C 372	18	1.4 143863	2	AC105649	Rattus no	C 445	18	1.4 192422	2	AC021071	AC021071 Homo sapi
C 373	18	1.4 146674	2	AC104397	Rattus no	C 446	18	1.4 194752	2	AC093349	AC093349 Mus muscu
C 374	18	1.4 147260	2	AC016340	Homo sapi	C 447	18	1.4 196087	2	AC106752	AC106752 Homo sapi
C 375	18	1.4 148123	2	AC098972	Homo sapi	C 448	18	1.4 197730	2	AC019094	AC019094 Homo sapi
C 376	18	1.4 148387	2	AC107015	Homo sapi	C 449	18	1.4 200286	2	AC079330	AC079330 Homo sapi
C 377	18	1.4 148670	2	AC024287	Homo sapi	C 450	18	1.4 200842	2	AC096319	AC096319 Rattus no
C 378	18	1.4 150430	2	AC016329	Homo sapi	C 451	18	1.4 208532	2	AP001460	AP001460 Homo sapi
C 379	18	1.4 152123	2	AC046190	Homo sapi	C 452	18	1.4 216161	2	AC094548	AC094548 Rattus no
C 380	18	1.4 152614	2	AC044881	Homo sapi	C 453	18	1.4 222068	2	AC087188	AC087188 Homo sapi
C 381	18	1.4 153576	2	AC020572	Homo sapi	C 454	18	1.4 224040	2	AC023174	AC023174 Mus muscu
C 382	18	1.4 153604	2	AC022754	Homo sapi	C 455	18	1.4 229518	2	AC069058	AC069058 Homo sapi
C 383	18	1.4 154936	2	AC021252	Homo sapi	C 456	18	1.4 229612	2	AL161647	AL161647 Homo sapi
C 384	18	1.4 154974	2	AC015481	Homo sapi	C 457	18	1.4 232240	2	AC095601	AC095601 Rattus no
C 385	18	1.4 156979	2	AC105635	Rattus no	C 458	18	1.4 234498	2	AC021077	AC021077 Homo sapi
C 386	18	1.4 157001	2	CNS07EF5	AL513356 Homo sapi	C 459	18	1.4 237181	2	AC023460	AC023460 Homo sapi
C 387	18	1.4 158078	2	AC095565	Rattus no	C 460	18	1.4 240021	2	AC099436	AC099436 Rattus no
C 388	18	1.4 158142	2	AL357130	Homo sapi	C 461	18	1.4 242396	2	AC098560	AC098560 Rattus no
C 389	18	1.4 158437	2	AL357130	Homo sapi	C 462	18	1.4 244530	2	AC097044	AC097044 Rattus no
C 390	18	1.4 159478	2	AL359638	Homo sapi	C 463	18	1.4 284207	2	AC103329	AC103329 Rattus no
C 391	18	1.4 160839	2	AC069257	Homo sapi	C 464	18	1.4 294090	2	AC096361	AC096361 Rattus no
C 392	18	1.4 162022	2	AC106425	Rattus no	C 465	18	1.4 302300	2	AP003186	AP003186 Clostridi
C 393	18	1.4 163077	2	AC027095	Homo sapi	C 466	17	1.3 74	6	AX342576	AX342576 Sequence
C 394	18	1.4 163229	2	AC015587	Homo sapi	C 467	17	1.3 74	6	AX342577	AX342577 Sequence
C 395	18	1.4 163388	2	AC096078	Rattus no	C 468	17	1.3 164	9	HS1307051	Z96276 H. sapiens t
C 396	18	1.4 163901	2	AC106426	Rattus no	C 469	17	1.3 262	11	G07021	G07021 human SRS W
C 397	18	1.4 164086	2	AC097929	Rattus no	C 470	17	1.3 302	5	TNICYTBAG	TNICYTBAG
C 398	18	1.4 165057	2	AC094471	Rattus no	C 471	17	1.3 362	11	AU029108	AU029108
C 399	18	1.4 165159	2	AC106643	Rattus no	C 472	17	1.3 400	11	G11048	G11048 human SRS S
C 400	18	1.4 165182	2	AC106300	Rattus no	C 473	17	1.3 446	11	G08878	G08878 human SRS C
C 401	18	1.4 165454	2	AC094051	Rattus no	C 474	17	1.3 581	11	G15788	G15788 human SRS C
C 402	18	1.4 165811	2	AC106276	Rattus no	C 475	17	1.3 644	9	HS4331225	AJ331225 Homo sapi
C 403	18	1.4 166885	2	AL353601	Homo sapi	C 476	17	1.3 650	11	AU046587	AU046587 Rattus no
C 404	18	1.4 167052	2	AL356058	Homo sapi	C 477	17	1.3 681	9	HS4542633	HS4542633
C 405	18	1.4 167871	2	AC099705	Mus muscu	C 478	17	1.3 682	11	G40740	G40740 Zebra
C 406	18	1.4 168259	2	AC067842	Homo sapi	C 479	17	1.3 755	6	AX268833	AX268833 Sequence
C 407	18	1.4 168414	2	AC023146	Homo sapi	C 480	17	1.3 922	8	HS4343374	AJ33374 Homo sapi
C 408	18	1.4 170163	2	AC064844	Homo sapi	C 481	17	1.3 923	5	HS434225	AJ334225 Homo sapi
C 409	18	1.4 170432	2	AC023322	Homo sapi	C 482	17	1.3 935	5	EU049343	EU049343 Emoia cyanu
C 410	18	1.4 170879	2	AC098135	Rattus no	C 483	17	1.3 942	9	HS433374	AJ33374 Homo sapi
C 411	18	1.4 170893	2	AC027537	Homo sapi	C 484	17	1.3 966	9	AY005661	AY005661 Homo sapi
C 412	18	1.4 171411	2	AC087609	Homo sapi	C 485	17	1.3 1280	6	A97486	A97486 Sequence 42
C 413	18	1.4 171423	2	AC025664	Homo sapi	C 486	17	1.3 1359	8	HS433385	AJ33385 Homo sapi
C 414	18	1.4 173263	2	AC106339	Rattus no	C 487	17	1.3 1362	8	AF0933720	AF0933720 Clitacaest
C 415	18	1.4 173976	2	AC073045	Homo sapi	C 488	17	1.3 1372	8	AF344571	AF344571 Peixotoa
C 416	18	1.4 174033	2	AC021957	Homo sapi	C 489	17	1.3 1428	8	AXU50230	AXU50230 Astrantia x
C 417	18	1.4 175040	2	AC106297	Rattus no	C 490	17	1.3 1428	8	EFU50234	EFU50234 Eremocharis
C 418	18	1.4 175569	2	AP001151	Homo sapi	C 491	17	1.3 1428	8	MM050247	MM050247 MacInlaya
C 419	18	1.4 175694	2	AC098134	Rattus no	C 492	17	1.3 1434	8	AF344534	AF344534 Burdachia
C 420	18	1.4 177206	2	AC098132	Rattus no	C 493	17	1.3 1521	6	AX255854	AX255854 Sequence
C 421	18	1.4 177731	2	AC018937	Homo sapi	C 494	17	1.3 2057	6	AX255854	AX255854 Sequence
C 422	18	1.4 178670	2	AC009290	Homo sapi	C 495	17	1.3 8553	2	AC091068	AC091068 Homo sapi
C 423	18	1.4 179439	2	AC018874	Homo sapi	C 496	17	1.3 8636	2	AC109674	AC109674 Rattus no
C 424	18	1.4 179775	2	AC103452	Rattus no	C 497	17	1.3 15313	2	AC101337	AC101337 Mus muscu
C 425	18	1.4 179989	2	AC016451	Homo sapi	C 498	17	1.3 16126	2	AC098350	AC098350 Rattus no
C 426	18	1.4 180583	2	AC098623	Rattus no	C 499	17	1.3 16289	2	AC090926	AC090926 Homo sapi
C 427	18	1.4 181029	30	AC026901	Homo sapi	C 500	17	1.3 19555	2	AC108649	AC108649 Rattus no
C 428	18	1.4 181921	2	AC098525	Rattus no	C 501	17	1.3 25770	2	AC110323	AC110323 Rattus no
C 429	18	1.4 181925	2	AC020710	Homo sapi	C 502	17	1.3 25967	2	AC100971	AC100971 Mus muscu
C 430	18	1.4 182299	2	AC023004	Homo sapi	C 503	17	1.3 29868	2	AC100539	AC100539 Mus muscu
C 431	18	1.4 182386	2	AC021990	Homo sapi	C 504	17	1.3 30389	2	AC103651	AC103651 Mus muscu
C 432	18	1.4 182795	2	AC010304	Rattus no	C 505	17	1.3 30620	2	AC104357	AC104357 Homo sapi
C 433	18	1.4 183355	2	AC021801	Homo sapi	C 506	17	1.3 32151	2	AC110407	AC110407 Rattus no
C 434	18	1.4 183624	2	AL512588	Mus muscu	C 507	17	1.3 32421	2	CEH25F02	CEH25F02 Caenorhabdi
C 435	18	1.4 184402	2	AC074199	Homo sapi	C 508	17	1.3 32785	2	AC013560	AC013560 Homo sapi
C 436	18	1.4 184635	2	AC025827	Homo sapi	C 509	17	1.3 32812	2	AC094250	AC094250 Rattus no
C 437	18	1.4 184826	2	AC009661	Homo sapi	C 510	17	1.3 33505	2	AC103634	AC103634 Mus muscu
C 438	18	1.4 185178	2	AP000937	Homo sapi	C 511	17	1.3 33751	2	AC099966	AC099966 Mus muscu

c 512	17	1.3	34563	2	AC109507	AC109507	Mus muscu	c 585	17	1.3	53026	2	AC104262	AC104262	Homo sapi
c 513	17	1.3	34753	2	AC104199	AC104199	Mus muscu	c 586	17	1.3	53128	2	AC068237	AC068237	Homo sapi
c 514	17	1.3	36021	2	AC087524	AC087524	Homo sapi	c 587	17	1.3	53149	2	AC110188	AC110188	Mus muscu
c 515	17	1.3	37034	2	AC102928	AC102928	Mus muscu	c 588	17	1.3	53714	2	AC101798	AC101798	Mus muscu
c 516	17	1.3	38271	2	AC100969	AC100969	Mus muscu	c 589	17	1.3	53967	2	AC012422	AC012422	Homo sapi
c 517	17	1.3	38316	2	AC008418	AC008418	Homo sapi	c 590	17	1.3	54134	2	AC101244	AC101244	Mus muscu
c 518	17	1.3	38562	2	AC097942	AC097942	Rattus no	c 591	17	1.3	54361	2	AC109178	AC109178	Mus muscu
c 519	17	1.3	38962	2	AC109503	AC109503	Mus muscu	c 592	17	1.3	54402	2	AC103361	AC103361	Mus muscu
c 520	17	1.3	39062	2	AC107880	AC107880	Homo sapi	c 593	17	1.3	54551	2	AC108808	AC108808	Mus muscu
c 521	17	1.3	39109	2	AC025107	AC025107	Homo sapi	c 594	17	1.3	54505	2	AC103155	AC103155	Rattus no
c 522	17	1.3	39935	2	AC107145	AC107145	Rattus no	c 595	17	1.3	54706	2	AC100048	AC100048	Mus muscu
c 523	17	1.3	39986	2	AC105174	AC105174	Mus muscu	c 596	17	1.3	54898	2	AC101851	AC101851	Mus muscu
c 524	17	1.3	40156	2	AC100852	AC100852	Homo sapi	c 597	17	1.3	54958	2	AC087405	AC087405	Homo sapi
c 525	17	1.3	40858	2	AC021816	AC021816	Homo sapi	c 598	17	1.3	55041	2	AC100046	AC100046	Mus muscu
c 526	17	1.3	41062	2	AC109290	AC109290	Mus muscu	c 599	17	1.3	55096	2	AC100894	AC100894	Mus muscu
c 527	17	1.3	41107	2	AC025943	AC025943	Homo sapi	c 600	17	1.3	55179	2	AC109255	AC109255	Mus muscu
c 528	17	1.3	41132	2	AC022741	AC022741	Homo sapi	c 601	17	1.3	55210	2	AC109257	AC109257	Mus muscu
c 529	17	1.3	41361	2	AC100106	AC100106	Mus muscu	c 602	17	1.3	55217	2	AC101358	AC101358	Mus muscu
c 530	17	1.3	41623	2	AC109253	AC109253	Mus muscu	c 603	17	1.3	55276	2	AC108425	AC108425	Mus muscu
c 531	17	1.3	41656	2	AC100134	AC100134	Mus muscu	c 604	17	1.3	55495	2	AC084007	AC084007	Homo sapi
c 532	17	1.3	41701	2	AC108634	AC108634	Rattus no	c 605	17	1.3	55518	2	AC110525	AC110525	Mus muscu
c 533	17	1.3	41724	2	AC110226	AC110226	Mus muscu	c 606	17	1.3	55742	2	AC087529	AC087529	Homo sapi
c 534	17	1.3	42241	2	CER0886	298854	Caenorhabdi	c 607	17	1.3	55823	2	AC040923	AC040923	Homo sapi
c 535	17	1.3	42271	2	AC100593	AC100593	Mus muscu	c 608	17	1.3	55884	2	AC108857	AC108857	Mus muscu
c 536	17	1.3	42722	2	AC015870	AC015870	Homo sapi	c 609	17	1.3	55943	2	AC087375	AC087375	Homo sapi
c 537	17	1.3	42849	2	AC107465	AC107465	Rattus no	c 610	17	1.3	55961	2	AC027765	AC027765	Homo sapi
c 538	17	1.3	43041	2	AC100149	AC100149	Mus muscu	c 611	17	1.3	56069	2	AC018631	AC018631	Drosophil
c 539	17	1.3	43201	2	AC100867	AC100867	Homo sapi	c 612	17	1.3	56292	2	AC109292	AC109292	Mus muscu
c 540	17	1.3	43638	2	AC015882	AC015882	Homo sapi	c 613	17	1.3	56336	2	AC101931	AC101931	Mus muscu
c 541	17	1.3	43902	2	AC010508	AC010508	Homo sapi	c 614	17	1.3	56559	2	AC008294	AC008294	Drosophil
c 542	17	1.3	44261	2	AC099891	AC099891	Mus muscu	c 615	17	1.3	56622	2	AC107997	AC107997	Homo sapi
c 543	17	1.3	44350	2	AC105099	AC105099	Homo sapi	c 616	17	1.3	56678	2	AC109254	AC109254	Mus muscu
c 544	17	1.3	44437	2	AC100102	AC100102	Mus muscu	c 617	17	1.3	56765	2	AC109227	AC109227	Mus muscu
c 545	17	1.3	44693	2	AC087338	AC087338	Homo sapi	c 618	17	1.3	56865	2	AC110186	AC110186	Mus muscu
c 546	17	1.3	44876	2	AC094172	AC094172	Rattus no	c 619	17	1.3	57051	2	AC084331	AC084331	Homo sapi
c 547	17	1.3	44988	2	AC106830	AC106830	Mus muscu	c 620	17	1.3	57109	2	AC060767	AC060767	Homo sapi
c 548	17	1.3	45210	2	AC087043	AC087043	Homo sapi	c 621	17	1.3	57144	2	AC100329	AC100329	Mus muscu
c 549	17	1.3	45809	2	AC016265	AC016265	Homo sapi	c 622	17	1.3	57144	2	AC108399	AC108399	Mus muscu
c 550	17	1.3	45912	2	AC091265	AC091265	Mus muscu	c 623	17	1.3	57275	2	AC074076	AC074076	Homo sapi
c 551	17	1.3	46555	2	AC100621	AC100621	Mus muscu	c 624	17	1.3	57293	2	AC079970	AC079970	Homo sapi
c 552	17	1.3	46579	2	AC109575	AC109575	Rattus no	c 625	17	1.3	57513	2	AC098434	AC098434	Rattus no
c 553	17	1.3	46690	2	AC100929	AC100929	Mus muscu	c 626	17	1.3	57518	2	AC101133	AC101133	Mus muscu
c 554	17	1.3	47043	2	AC109219	AC109219	Mus muscu	c 627	17	1.3	57586	2	AC110232	AC110232	Mus muscu
c 555	17	1.3	47226	2	AC105215	AC105215	Homo sapi	c 628	17	1.3	57655	2	AC100690	AC100690	Mus muscu
c 556	17	1.3	47850	2	AC100503	AC100503	Mus muscu	c 629	17	1.3	57730	2	AC108858	AC108858	Mus muscu
c 557	17	1.3	48818	2	AC102557	AC102557	Mus muscu	c 630	17	1.3	57877	2	AC100077	AC100077	Mus muscu
c 558	17	1.3	49063	2	AC101842	AC101842	Mus muscu	c 631	17	1.3	57900	2	AC106829	AC106829	Mus muscu
c 559	17	1.3	49084	2	AC106019	AC106019	Homo sapi	c 632	17	1.3	58058	2	AC105992	AC105992	Mus muscu
c 560	17	1.3	49105	2	AC067787	AC067787	Homo sapi	c 633	17	1.3	58258	2	AC100828	AC100828	Homo sapi
c 561	17	1.3	49393	2	AC104565	AC104565	Homo sapi	c 634	17	1.3	58274	2	AC084092	AC084092	Homo sapi
c 562	17	1.3	49535	2	AC100334	AC100334	Mus muscu	c 635	17	1.3	58288	2	AC101021	AC101021	Mus muscu
c 563	17	1.3	49802	2	AC102893	AC102893	Mus muscu	c 636	17	1.3	58496	2	AC101077	AC101077	Mus muscu
c 564	17	1.3	50028	2	AC105330	AC105330	Mus muscu	c 637	17	1.3	58517	2	AC101002	AC101002	Mus muscu
c 565	17	1.3	50132	2	AC104753	AC104753	Mus muscu	c 638	17	1.3	58536	2	AC109274	AC109274	Mus muscu
c 566	17	1.3	50165	2	AC101877	AC101877	Mus muscu	c 639	17	1.3	58547	2	AC110215	AC110215	Mus muscu
c 567	17	1.3	50224	2	AC110157	AC110157	Mus muscu	c 640	17	1.3	58552	2	AC110552	AC110552	Mus muscu
c 568	17	1.3	50500	2	AC100432	AC100432	Mus muscu	c 641	17	1.3	58623	2	AC101064	AC101064	Mus muscu
c 569	17	1.3	50699	2	AC107468	AC107468	Rattus no	c 642	17	1.3	58636	2	AC109164	AC109164	Mus muscu
c 570	17	1.3	50725	2	AC109177	AC109177	Mus muscu	c 643	17	1.3	58693	2	AC107875	AC107875	Homo sapi
c 571	17	1.3	50738	2	AC091080	AC091080	Homo sapi	c 644	17	1.3	58828	2	AC090931	AC090931	Homo sapi
c 572	17	1.3	50930	2	AC107974	AC107974	Homo sapi	c 645	17	1.3	58879	2	AC090350	AC090350	Homo sapi
c 573	17	1.3	51668	2	AC108819	AC108819	Mus muscu	c 646	17	1.3	58901	2	AC102509	AC102509	Mus muscu
c 574	17	1.3	51820	2	AC099967	AC099967	Mus muscu	c 647	17	1.3	58902	2	AC102053	AC102053	Mus muscu
c 575	17	1.3	51832	2	AC101875	AC101875	Mus muscu	c 648	17	1.3	58970	2	AC011863	AC011863	Homo sapi
c 576	17	1.3	51882	2	AC107846	AC107846	Mus muscu	c 649	17	1.3	59013	2	AC102793	AC102793	Mus muscu
c 577	17	1.3	51918	2	AC104201	AC104201	Mus muscu	c 650	17	1.3	59043	2	AC100881	AC100881	Mus muscu
c 578	17	1.3	52000	2	AC101348	AC101348	Mus muscu	c 651	17	1.3	59147	2	AC100014	AC100014	Mus muscu
c 579	17	1.3	52122	2	AC011861	AC011861	Homo sapi	c 652	17	1.3	59205	2	AC084254	AC084254	Homo sapi
c 580	17	1.3	52290	2	AC025314	AC025314	Homo sapi	c 653	17	1.3	59219	2	AC090585	AC090585	Homo sapi
c 581	17	1.3	52359	2	AC101072	AC101072	Homo sapi	c 654	17	1.3	59247	2	AC015645	AC015645	Homo sapi
c 582	17	1.3	52675	2	AC103409	AC103409	Homo sapi	c 655	17	1.3	59446	2	AC099952	AC099952	Mus muscu
c 583	17	1.3	52840	2	AC101934	AC101934	Mus muscu	c 656	17	1.3	59461	2	AC011889	AC011889	Homo sapi
c 584	17	1.3	52947	2	AC068354	AC068354	Homo sapi	c 657	17	1.3	59469	2	AC101150	AC101150	Mus muscu

c 658	17	1.3	59663	2	AC107241	Homo sapi	c 731	17	1.3	64737	2	AC104382	AC104382	Homo sapi
c 659	17	1.3	59806	2	AC102351	Mus muscu	c 732	17	1.3	64800	2	AC101863	AC101863	Mus muscu
c 660	17	1.3	60004	2	AC103601	AC1013601	c 733	17	1.3	64835	2	AC102214	AC102214	Mus muscu
c 661	17	1.3	60031	2	AC087670	AC087670	c 734	17	1.3	64855	2	AC102468	AC102468	Mus muscu
c 662	17	1.3	60079	2	AC100183	AC100183	c 735	17	1.3	65000	2	AC090238	AC090238	Mus muscu
c 663	17	1.3	60116	2	AC109238	AC109238	c 736	17	1.3	65000	2	AC100041	AC100041	Mus muscu
c 664	17	1.3	60136	2	AC087480	AC087480	c 737	17	1.3	65053	2	AC101795	AC101795	Mus muscu
c 665	17	1.3	60322	2	AC099885	AC099885	c 738	17	1.3	65076	2	AC110538	AC110538	Mus muscu
c 666	17	1.3	60481	2	AC102766	AC102766	c 739	17	1.3	65112	2	AC100982	AC100982	Mus muscu
c 667	17	1.3	60505	2	AC105965	AC105965	c 740	17	1.3	65252	2	AC110176	AC110176	Mus muscu
c 668	17	1.3	60580	2	AC101218	AC101218	c 741	17	1.3	65264	2	AC100794	AC100794	Mus muscu
c 669	17	1.3	60685	2	AC104355	AC104355	c 742	17	1.3	65280	2	AC100898	AC100898	Mus muscu
c 670	17	1.3	60928	2	AC103830	AC103830	c 743	17	1.3	65347	2	AC102307	AC102307	Mus muscu
c 671	17	1.3	60938	2	AC101380	AC101380	c 744	17	1.3	65348	2	AC102338	AC102338	Mus muscu
c 672	17	1.3	60967	2	AC100246	AC100246	c 745	17	1.3	65389	2	AC107730	AC107730	Mus muscu
c 673	17	1.3	60972	2	AC101241	AC101241	c 746	17	1.3	65434	2	AC101467	AC101467	Mus muscu
c 674	17	1.3	61006	2	AC104001	AC104001	c 747	17	1.3	65462	2	AC102517	AC102517	Mus muscu
c 675	17	1.3	61006	2	AC104001	AC104001	c 748	17	1.3	65478	2	AC101944	AC101944	Mus muscu
c 676	17	1.3	61138	2	AC110544	AC110544	c 749	17	1.3	65493	2	AC102851	AC102851	Mus muscu
c 677	17	1.3	61146	2	AC101242	AC101242	c 750	17	1.3	65531	2	AC102187	AC102187	Mus muscu
c 678	17	1.3	61173	2	AC107945	AC107945	c 751	17	1.3	65530	2	AC011923	AC011923	Mus muscu
c 679	17	1.3	61175	2	AC110263	AC110263	c 752	17	1.3	65599	2	AC090782	AC090782	Mus muscu
c 680	17	1.3	61232	2	AC084029	AC084029	c 753	17	1.3	65624	2	AC109176	AC109176	Mus muscu
c 681	17	1.3	61251	2	AC101771	AC101771	c 754	17	1.3	65638	2	AC068516	AC068516	Mus muscu
c 682	17	1.3	61368	2	AC101337	AC101337	c 755	17	1.3	65690	2	AC107752	AC107752	Mus muscu
c 683	17	1.3	61383	2	AC110542	AC110542	c 756	17	1.3	65755	2	AC011160	AC011160	Mus muscu
c 684	17	1.3	61490	2	AC025630	AC025630	c 757	17	1.3	65806	2	AC102410	AC102410	Mus muscu
c 685	17	1.3	61536	2	AC103721	AC103721	c 758	17	1.3	65816	2	AC105194	AC105194	Mus muscu
c 686	17	1.3	61559	2	AC080045	AC080045	c 759	17	1.3	65878	2	AC090767	AC090767	Mus muscu
c 687	17	1.3	61802	2	AC101970	AC101970	c 760	17	1.3	65892	2	AC103599	AC103599	Mus muscu
c 688	17	1.3	61830	2	AC100979	AC100979	c 761	17	1.3	65969	2	AC101741	AC101741	Mus muscu
c 689	17	1.3	61925	2	AC101834	AC101834	c 762	17	1.3	66047	2	AC110272	AC110272	Mus muscu
c 690	17	1.3	61940	2	AC109312	AC109312	c 763	17	1.3	66074	2	AC101807	AC101807	Mus muscu
c 691	17	1.3	62077	2	AC027091	AC027091	c 764	17	1.3	66084	2	AC100383	AC100383	Mus muscu
c 692	17	1.3	62105	2	AC084139	AC084139	c 765	17	1.3	66086	2	AC101249	AC101249	Mus muscu
c 693	17	1.3	62198	2	AC013832	AC013832	c 766	17	1.3	66111	2	AC101740	AC101740	Mus muscu
c 694	17	1.3	62271	2	AC100214	AC100214	c 767	17	1.3	66137	2	AC101526	AC101526	Mus muscu
c 695	17	1.3	62289	2	AC102411	AC102411	c 768	17	1.3	66152	2	AC090613	AC090613	Mus muscu
c 696	17	1.3	62305	2	AC090546	AC090546	c 769	17	1.3	66191	2	AC107608	AC107608	Mus muscu
c 697	17	1.3	62379	2	AC102721	AC102721	c 770	17	1.3	66227	2	AC026534	AC026534	Rattus no
c 698	17	1.3	62466	2	AC083998	AC083998	c 771	17	1.3	66330	2	AC101316	AC101316	Mus muscu
c 699	17	1.3	62470	2	AC015828	AC015828	c 772	17	1.3	66334	2	AC102196	AC102196	Mus muscu
c 700	17	1.3	62501	2	AC101332	AC101332	c 773	17	1.3	66348	2	AC025016	AC025016	Mus muscu
c 701	17	1.3	62722	2	AC100493	AC100493	c 774	17	1.3	66393	2	AC100424	AC100424	Mus muscu
c 702	17	1.3	62723	2	AC100651	AC100651	c 775	17	1.3	66415	2	AC105323	AC105323	Mus muscu
c 703	17	1.3	62765	2	AC100216	AC100216	c 776	17	1.3	66442	2	AC101865	AC101865	Mus muscu
c 704	17	1.3	62846	2	AC084174	AC084174	c 777	17	1.3	66489	2	AC100766	AC100766	Mus muscu
c 705	17	1.3	62894	2	AC069167	AC069167	c 778	17	1.3	66505	2	AC102041	AC102041	Mus muscu
c 706	17	1.3	62954	2	AC102036	AC102036	c 779	17	1.3	66506	2	AP001861	AP001861	Mus muscu
c 707	17	1.3	63064	2	AC103940	AC103940	c 780	17	1.3	66733	2	AC090663	AC090663	Mus muscu
c 708	17	1.3	63100	2	AC103936	AC103936	c 781	17	1.3	66736	2	AC100221	AC100221	Mus muscu
c 709	17	1.3	63398	2	AC102456	AC102456	c 782	17	1.3	66737	2	AC103828	AC103828	Mus muscu
c 710	17	1.3	63527	2	AC102605	AC102605	c 783	17	1.3	66797	2	AC084718	AC084718	Mus muscu
c 711	17	1.3	63540	2	AC101468	AC101468	c 784	17	1.3	66836	2	AC016492	AC016492	Mus muscu
c 712	17	1.3	63600	2	AC101405	AC101405	c 785	17	1.3	66850	2	AC103808	AC103808	Mus muscu
c 713	17	1.3	63632	2	AC108792	AC108792	c 786	17	1.3	66868	2	AC069377	AC069377	Mus muscu
c 714	17	1.3	63739	2	AC087621	AC087621	c 787	17	1.3	66871	2	AC108790	AC108790	Mus muscu
c 715	17	1.3	63739	2	AC102458	AC102458	c 788	17	1.3	66902	2	AC107799	AC107799	Mus muscu
c 716	17	1.3	63769	2	AC079334	AC079334	c 789	17	1.3	67024	2	AC102715	AC102715	Mus muscu
c 717	17	1.3	63847	2	AC101459	AC101459	c 790	17	1.3	67047	2	AC103544	AC103544	Mus muscu
c 718	17	1.3	63880	2	AC100897	AC100897	c 791	17	1.3	67059	2	AC103779	AC103779	Mus muscu
c 719	17	1.3	63928	2	AC100290	AC100290	c 792	17	1.3	67100	2	AC101767	AC101767	Mus muscu
c 720	17	1.3	63959	2	AC107833	AC107833	c 793	17	1.3	67105	2	AC104033	AC104033	Mus muscu
c 721	17	1.3	64114	2	AC104944	AC104944	c 794	17	1.3	67176	2	AC101326	AC101326	Mus muscu
c 722	17	1.3	64117	2	AC110571	AC110571	c 795	17	1.3	67214	2	AC101561	AC101561	Mus muscu
c 723	17	1.3	64164	2	AC099948	AC099948	c 796	17	1.3	67292	2	AC102708	AC102708	Mus muscu
c 724	17	1.3	64366	2	AC103635	AC103635	c 797	17	1.3	67322	2	AC102007	AC102007	Mus muscu
c 725	17	1.3	64393	2	AC110036	AC110036	c 798	17	1.3	67338	2	AC101463	AC101463	Mus muscu
c 726	17	1.3	64533	2	AC103843	AC103843	c 799	17	1.3	67349	2	AC102316	AC102316	Mus muscu
c 727	17	1.3	64573	2	AC100511	AC100511	c 800	17	1.3	67378	2	AC110028	AC110028	Mus muscu
c 728	17	1.3	64628	2	AC100288	AC100288	c 801	17	1.3	67499	2	AC101967	AC101967	Mus muscu
c 729	17	1.3	64634	2	AC100010	AC100010	c 802	17	1.3	67644	2	AC100474	AC100474	Mus muscu
c 730	17	1.3	64695	2	AC101555	AC101555	c 803	17	1.3	67676	2	AC090161	AC090161	Mus muscu

804	17	1.3	67722	2	AC087747	AC087747	Homo sapi	C 877	17	1.3	71482	2	HSNS6B8	299132	Homo sapien
C 805	17	1.3	67724	2	AC102164	AC102164	Mus muscu	C 878	17	1.3	71511	2	AC103753	AC103753	Homo sapi
C 806	17	1.3	67726	2	AC101220	AC101220	Mus muscu	C 879	17	1.3	71614	2	AC102274	AC102274	Mus muscu
C 807	17	1.3	67811	2	AC102396	AC102396	Mus muscu	C 880	17	1.3	71663	2	AC101513	AC101513	Mus muscu
C 808	17	1.3	67850	2	AC100568	AC100568	Mus muscu	C 881	17	1.3	71663	2	AC101513	AC101513	Mus muscu
C 809	17	1.3	67943	2	AC101108	AC101108	Mus muscu	C 882	17	1.3	71744	2	AC100638	AC100638	Mus muscu
C 810	17	1.3	68052	2	AC100691	AC100691	Mus muscu	C 883	17	1.3	71823	2	AC104962	AC104962	Mus muscu
C 811	17	1.3	68165	2	AC099913	AC099913	Mus muscu	C 884	17	1.3	71913	2	AC104890	AC104890	Mus muscu
C 812	17	1.3	68224	2	AC100167	AC100167	Mus muscu	C 885	17	1.3	71919	2	AC102117	AC102117	Mus muscu
C 813	17	1.3	68238	2	AC100380	AC100380	Mus muscu	C 886	17	1.3	72321	2	AC101399	AC101399	Mus muscu
C 814	17	1.3	68248	2	AC090295	AC090295	Mus muscu	C 887	17	1.3	72363	2	AC101353	AC101353	Mus muscu
C 815	17	1.3	68402	2	AC100370	AC100370	Mus muscu	C 888	17	1.3	72539	2	AC101775	AC101775	Mus muscu
C 816	17	1.3	68418	2	AC106111	AC106111	Rattus no	C 889	17	1.3	72612	2	AC102056	AC102056	Mus muscu
C 817	17	1.3	68443	2	AC100869	AC100869	Homo sapi	C 890	17	1.3	72757	2	AC025301	AC025301	Mus muscu
C 818	17	1.3	68555	2	AC104963	AC104963	Homo sapi	C 891	17	1.3	72828	2	AC103606	AC103606	Homo sapi
C 819	17	1.3	68562	2	AC104936	AC104936	Homo sapi	C 892	17	1.3	72829	2	AC090688	AC090688	Mus muscu
C 820	17	1.3	68591	2	AC107771	AC107771	Mus muscu	C 893	17	1.3	72865	2	AC102123	AC102123	Mus muscu
C 821	17	1.3	68665	2	AC102122	AC102122	Mus muscu	C 894	17	1.3	72871	2	AC091550	AC091550	Mus muscu
C 822	17	1.3	68675	2	AC100160	AC100160	Mus muscu	C 895	17	1.3	72942	2	AC101409	AC101409	Mus muscu
C 823	17	1.3	68694	2	AC095414	AC095414	Mus muscu	C 896	17	1.3	73027	2	AC101911	AC101911	Mus muscu
C 824	17	1.3	68850	2	AC015606	AC015606	Rattus no	C 897	17	1.3	73356	2	AC102678	AC102678	Mus muscu
C 825	17	1.3	68862	2	AC101828	AC101828	Mus muscu	C 898	17	1.3	73397	2	AC101427	AC101427	Mus muscu
C 826	17	1.3	68872	2	AC103726	AC103726	Mus muscu	C 899	17	1.3	73424	2	AC102049	AC102049	Mus muscu
C 827	17	1.3	68873	2	AC101531	AC101531	Mus muscu	C 900	17	1.3	73435	2	AC091015	AC091015	Homo sapi
C 828	17	1.3	68949	2	AC102600	AC102600	Mus muscu	C 901	17	1.3	73594	2	AC087268	AC087268	Homo sapi
C 829	17	1.3	68993	2	AC102296	AC102296	Mus muscu	C 902	17	1.3	73629	2	AC101616	AC101616	Mus muscu
C 830	17	1.3	69009	2	AC104932	AC104932	Mus muscu	C 903	17	1.3	73638	2	AC101821	AC101821	Mus muscu
C 831	17	1.3	69111	2	AC102167	AC102167	Mus muscu	C 904	17	1.3	73648	2	AC109187	AC109187	Mus muscu
C 832	17	1.3	69133	2	AC110508	AC110508	Mus muscu	905	17	1.3	73684	2	AC101199	AC101199	Mus muscu
C 833	17	1.3	69156	2	AC090542	AC090542	Homo sapi	906	17	1.3	73689	2	AC101783	AC101783	Mus muscu
C 834	17	1.3	69178	2	AC101217	AC101217	Mus muscu	C 907	17	1.3	73742	2	AC101946	AC101946	Mus muscu
C 835	17	1.3	69238	2	AC090784	AC090784	Homo sapi	C 908	17	1.3	73880	2	AC090728	AC090728	Mus muscu
C 836	17	1.3	69269	2	AC102533	AC102533	Mus muscu	C 909	17	1.3	73889	2	AC101573	AC101573	Mus muscu
C 837	17	1.3	69269	2	AC102533	AC102533	Mus muscu	C 910	17	1.3	73994	2	AC024314	AC024314	Homo sapi
C 838	17	1.3	69335	2	AC026485	AC026485	Homo sapi	C 911	17	1.3	74037	2	AC099843	AC099843	Homo sapi
C 839	17	1.3	69397	2	AC105070	AC105070	Mus muscu	C 912	17	1.3	74137	2	AC101636	AC101636	Mus muscu
C 840	17	1.3	69489	2	AC102134	AC102134	Mus muscu	C 913	17	1.3	74205	2	AC100921	AC100921	Mus muscu
C 841	17	1.3	69507	2	AC104909	AC104909	Mus muscu	C 914	17	1.3	74512	2	AC025641	AC025641	Homo sapi
C 842	17	1.3	69620	2	AC102374	AC102374	Mus muscu	C 915	17	1.3	74516	2	AC021746	AC021746	Homo sapi
C 843	17	1.3	69736	2	AC101257	AC101257	Mus muscu	C 916	17	1.3	74570	2	AC109229	AC109229	Mus muscu
C 844	17	1.3	69748	2	AC100129	AC100129	Mus muscu	C 917	17	1.3	74570	2	AC110018	AC110018	Homo sapi
C 845	17	1.3	69792	2	AC100887	AC100887	Mus muscu	C 918	17	1.3	74658	2	AC102175	AC102175	Mus muscu
C 846	17	1.3	69852	2	AC103750	AC103750	Mus muscu	C 919	17	1.3	74854	2	AC102185	AC102185	Mus muscu
C 847	17	1.3	69857	2	AC102687	AC102687	Mus muscu	C 920	17	1.3	75039	2	AC101585	AC101585	Mus muscu
C 848	17	1.3	69900	2	AC101433	AC101433	Mus muscu	C 921	17	1.3	75141	2	AC101848	AC101848	Drosophil
C 849	17	1.3	69926	2	AC102709	AC102709	Mus muscu	C 922	17	1.3	75162	2	AC102256	AC102256	Mus muscu
C 850	17	1.3	69930	2	AC103351	AC103351	Mus muscu	C 923	17	1.3	75282	2	DMBR37M19	DMBR37M19	Mus muscu
C 851	17	1.3	69947	2	AC102200	AC102200	Mus muscu	C 924	17	1.3	75330	2	AC101577	AC101577	Mus muscu
C 852	17	1.3	70089	2	AC027491	AC027491	Homo sapi	925	17	1.3	75337	2	AC101577	AC101577	Mus muscu
C 853	17	1.3	70145	2	AC100303	AC100303	Mus muscu	C 926	17	1.3	75446	2	AC084304	AC084304	Homo sapi
C 854	17	1.3	70202	2	AC101627	AC101627	Mus muscu	C 927	17	1.3	75493	2	AC015877	AC015877	Homo sapi
C 855	17	1.3	70212	2	AC103811	AC103811	Mus muscu	C 928	17	1.3	75581	2	AC103059	AC103059	Rattus no
C 856	17	1.3	70326	2	AC068957	AC068957	Homo sapi	C 929	17	1.3	75892	2	AC101297	AC101297	Mus muscu
C 857	17	1.3	70353	2	AC102616	AC102616	Mus muscu	C 930	17	1.3	76141	2	AC024393	AC024393	Homo sapi
C 858	17	1.3	70360	2	AC101122	AC101122	Mus muscu	C 931	17	1.3	76376	2	AC1021969	AC1021969	Homo sapi
C 859	17	1.3	70374	2	AC103935	AC103935	Mus muscu	932	17	1.3	76665	2	AC105818	AC105818	Rattus no
C 860	17	1.3	70386	2	AC1010264	AC1010264	Mus muscu	933	17	1.3	76986	2	AC067977	AC067977	Homo sapi
C 861	17	1.3	70485	2	AC104214	AC104214	Mus muscu	C 934	17	1.3	77772	2	AC027549	AC027549	Rattus no
C 862	17	1.3	70715	2	AC100513	AC100513	Mus muscu	C 935	17	1.3	77844	2	AC103437	AC103437	Homo sapi
C 863	17	1.3	70744	2	AC021508	AC021508	Homo sapi	C 936	17	1.3	78011	2	AC094328	AC094328	Rattus no
C 864	17	1.3	70830	2	AC101408	AC101408	Mus muscu	C 937	17	1.3	78553	2	AC094328	AC094328	Rattus no
C 865	17	1.3	70993	2	AC102199	AC102199	Mus muscu	C 938	17	1.3	78577	2	AC091376	AC091376	Rattus no
C 866	17	1.3	71008	2	AC080024	AC080024	Homo sapi	C 939	17	1.3	78974	2	AC025109	AC025109	Homo sapi
C 867	17	1.3	71077	2	AC100490	AC100490	Mus muscu	C 940	17	1.3	79037	2	AC016981	AC016981	Homo sapi
C 868	17	1.3	71130	2	AC103662	AC103662	Mus muscu	C 941	17	1.3	79544	2	AC016859	AC016859	Homo sapi
C 869	17	1.3	71134	2	AC011787	AC011787	Homo sapi	942	17	1.3	79874	2	AC027252	AC027252	Homo sapi
C 870	17	1.3	71142	2	AC016305	AC016305	Homo sapi	943	17	1.3	78692	2	AC100569	AC100569	Mus muscu
C 871	17	1.3	71215	2	AC026514	AC026514	Homo sapi	944	17	1.3	80692	2	AC095072	AC095072	Rattus no
C 872	17	1.3	71241	2	AC101454	AC101454	Mus muscu	945	17	1.3	80710	2	AC025618	AC025618	Homo sapi
C 873	17	1.3	71295	2	AC101292	AC101292	Mus muscu	946	17	1.3	80830	2	AC021244	AC021244	Homo sapi
C 874	17	1.3	71430	2	AC106039	AC106039	Homo sapi	C 947	17	1.3	81395	2	AC016475	AC016475	Homo sapi
C 875	17	1.3	71448	2	AC100361	AC100361	Mus muscu	948	17	1.3	81592	2	AC094271	AC094271	Rattus no
C 876	17	1.3	71454	2	AC100378	AC100378	Mus muscu	949	17	1.3	81880	2	AC096976	AC096976	Rattus no

950	17	1.3	82576	2	AC098147	Rattus no	AC098147	Rattus no	AC098147
C 951	17	1.3	82665	2	AC022304	Homo sapi	AC022304	Homo sapi	AC022304
C 952	17	1.3	82700	2	AC015635	Homo sapi	AC015635	Homo sapi	AC015635
C 953	17	1.3	83389	2	AC022802	Homo sapi	AC022802	Homo sapi	AC022802
C 954	17	1.3	83589	2	AC073402	Homo sapi	AC073402	Homo sapi	AC073402
C 955	17	1.3	84252	2	AC009207	Drosophila	AC009207	Drosophila	AC009207
C 956	17	1.3	84713	2	AC096788	Rattus no	AC096788	Rattus no	AC096788
C 957	17	1.3	85559	2	AC022892	Homo sapi	AC022892	Homo sapi	AC022892
C 958	17	1.3	86157	2	AC103014	Rattus no	AC103014	Rattus no	AC103014
C 959	17	1.3	86997	2	AC108364	Homo sapi	AC108364	Homo sapi	AC108364
C 960	17	1.3	88064	2	AC022707	Homo sapi	AC022707	Homo sapi	AC022707
C 961	17	1.3	88832	2	AC095921	Rattus no	AC095921	Rattus no	AC095921
C 962	17	1.3	89247	2	DBMR3H4	Drosophila	DBMR3H4	Drosophila	DBMR3H4
C 963	17	1.3	89388	2	AC102999	Rattus no	AC102999	Rattus no	AC102999
C 964	17	1.3	89631	2	AC096930	Rattus no	AC096930	Rattus no	AC096930
C 965	17	1.3	89710	2	DBMR3J311	Drosophila	DBMR3J311	Drosophila	DBMR3J311
C 966	17	1.3	90005	2	AC106630	Rattus no	AC106630	Rattus no	AC106630
C 967	17	1.3	90881	2	AC096486	Rattus no	AC096486	Rattus no	AC096486
C 968	17	1.3	91273	2	AC099277	Rattus no	AC099277	Rattus no	AC099277
C 969	17	1.3	91640	2	AC098041	Rattus no	AC098041	Rattus no	AC098041
C 970	17	1.3	91949	2	AC021254	Homo sapi	AC021254	Homo sapi	AC021254
C 971	17	1.3	92118	2	AC106613	Rattus no	AC106613	Rattus no	AC106613
C 972	17	1.3	92580	2	AC016302	Homo sapi	AC016302	Homo sapi	AC016302
C 973	17	1.3	92623	2	AC009684	Homo sapi	AC009684	Homo sapi	AC009684
C 974	17	1.3	93060	2	AC013499	Homo sapi	AC013499	Homo sapi	AC013499
C 975	17	1.3	93581	2	AC094226	Rattus no	AC094226	Rattus no	AC094226
C 976	17	1.3	93867	2	AC094139	Rattus no	AC094139	Rattus no	AC094139
C 977	17	1.3	94297	2	AC069584	Rattus no	AC069584	Rattus no	AC069584
C 978	17	1.3	94364	2	AC079048	Homo sapi	AC079048	Homo sapi	AC079048
C 979	17	1.3	95884	2	AC068839	Homo sapi	AC068839	Homo sapi	AC068839
C 980	17	1.3	96001	2	AC084096	Homo sapi	AC084096	Homo sapi	AC084096
C 981	17	1.3	96220	2	AC095683	Rattus no	AC095683	Rattus no	AC095683
C 982	17	1.3	96746	2	AC094998	Rattus no	AC094998	Rattus no	AC094998
C 983	17	1.3	96797	2	AC103256	Rattus no	AC103256	Rattus no	AC103256
C 984	17	1.3	97478	2	AC105929	Magnapor	AC105929	Magnapor	AC105929
C 985	17	1.3	98506	2	AC094918	Rattus no	AC094918	Rattus no	AC094918
C 986	17	1.3	99083	3	CEY37A1B	Caenorhab	ALU023835	Caenorhab	ALU023835
C 987	17	1.3	99213	2	AC106153	Rattus no	AC106153	Rattus no	AC106153
C 988	17	1.3	99392	2	AC105869	Rattus no	AC105869	Rattus no	AC105869
C 989	17	1.3	99956	2	AC097159	Rattus no	AC097159	Rattus no	AC097159
C 990	17	1.3	100712	2	AC097198	Rattus no	AC097198	Rattus no	AC097198
C 991	17	1.3	100931	2	AC094528	Rattus no	AC094528	Rattus no	AC094528
C 992	17	1.3	101041	2	AP002079	Homo sapi	AP002079	Homo sapi	AP002079
C 993	17	1.3	103117	2	AC108015	Homo sapi	AC108015	Homo sapi	AC108015
C 994	17	1.3	103904	8	ATAC021640	Aridiplops	AC008713	Homo sapi	AC008713
C 995	17	1.3	104514	2	AC105811	Rattus no	AC105811	Rattus no	AC105811
C 996	17	1.3	105562	2	AC105811	Rattus no	AC105811	Rattus no	AC105811
C 997	17	1.3	105768	2	AC105712	Rattus no	AC105712	Rattus no	AC105712
C 998	17	1.3	106676	2	AC011173	Homo sapi	AC011173	Homo sapi	AC011173
C 999	17	1.3	106676	2	AC011173	Homo sapi	AC011173	Homo sapi	AC011173
C 1000	17	1.3	106807	2	AC105431	Magnapor	AC105431	Magnapor	AC105431

ALIGNMENTS

RESULT	1																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																			
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FEATURES	Location/Qualifiers
Source	1. 1328 /organism="Staphylococcus sp." /db_xref="taxon:29387"
BASE COUNT	304 a 78 c 146 g 227 t 573 others
ORIGIN	
Query Match	100.0%; Score 1328; DB 6; Length 1328;
Best Local Similarity	100.0%; Pident. No. 0;
Matches 1328; Conservative	0; Mismatches 0; Indels 0; Gaps
OY	1 nnnnnnnnnnnnaaaatgaaatttcaacaaatttaacgcnagaaganttngnnntttac 60
DB	1 NNNNNNNNNNNNAATGAANTTTACAAATTTTACACNCANAGAGANTTNGCANNNTTAC 60
OY	61 ngannnaatgcnnaaagacattcaacacaaannngnnantlangannntaaanttgc 120
DB	61 NGANNNATGNCNNNAAGNCATTTCACCAVANNNNNGNNNANTANGANNNTAANTTGC 120
OY	121 nnaannnnngannccncaatagcttggnaatnaaanaaanaataangantttatgcgc 180
DB	121 NNAANNNNNGANNCCANNATAGTNGAATNAANAANNAANTATANGANTGATTCGNC 180
OY	181 ntgnattttaacngcngcncngtinaatgaaantttanaantcatttattcnaaangng 240
DB	181 NTGNATNTTACNGCNGCNGTATGAANTNTTNAANTNTTATTCNAANNNGG 240
OY	241 nccngtinaatgatttanaaanaanaagancctgttncantttcttaanganattmmaa 300
DB	241 NCCNGTNTAGATTTTNANAANNAAGCCTGTNCANTNTTCTTAAANGANTTNNNA 300
OY	301 ntaattnaaanaanaantttnnatctantnnnn ttgaacnctcanncttncataca 360
DB	301 NTATTTNAANAANNAANTTNNNTTATANTTNNNTGACNCTAANTTNCNTATCATATA 360
OY	361 nnnnaatcatgangaagannctnnnngnaatctgcnggnaangatttgnltttgtaant 420
DB	361 NNNNAATCATGANGANGANNNTNNNGNNAATGCGNGNNAAGATTGGTNTTGCATTANNT 420
OY	421 nnnnnnnntgnttttncanannnggtctttnnaanggtcttgancctnnncaaat 480
DB	421 NNNNNNNNTGCGNTTTNANCANNNGGTTTNNNNAANGGTTTGACNCTTNNNCAAT 480
OY	481 nngntncaantcngtntanaatttannnnnnnaaaannccnaagannctnntnaannnat 540
DB	481 NNGNTNNCAANTCNGTNTTANATTTANNNNNNNAAAAANNCCNANAGANNNTNTNAAANNAT 540
OY	541 ggatrgntttngnaannnaaanaacraaaaagttnaaanaaatgggttinaaagtnnnt 600
DB	541 GGATRGNTTNGGNAANNNAACRAAAAAGTTNAAANAAATGGNGTNAAGTNNNTT 600
OY	601 nntnnnnnaagangantctncaattttngttcatcttataiggangaatacncnganncaa 660
DB	601 NNTNNNNNAAGANGANTTNCNAATTTTNGGTCATTNTTGANGATACNNGCANGCNAA 660
OY	661 ngntctnnngatnganganannntcttantaanaangtctnnnnnatctnaaagann 720
DB	661 NGNTCTNNNGATNGANGANNTTNTTANTANANGGNTNNNNNATTTNAAAGANN 720
OY	721 ngttnttngtcnccngcngctatatnnaatttgatgtaacantttnnggaaatcnaannnga 780
DB	721 NGTNTTNGTNCNCGNTATATTNANTTTTTCATGANTANNTNNNGGAANTNNANNNGA 780
OY	781 nngnaannnnntnaataaagannnaaanaagcnn tnaaanaatnganaaangcncga 840
DB	781 NNGNNAANNNTNANTAAAGANNNAANAAGCNTTANANGANTNGANAANAONCCNGA 840
OY	841 naaanaaaagcnnnaaanaannnnnnnaaann tnaaanaaanttnngcnaaannca 900
DB	841 NAAANAAGCNNNAANNAANNNNNNNAANTTNAANAANCAANTNNNGCNAANNANCA 900
OY	901 aaantttnaangcngnaannnnnttnaaannnanaatcignaangaattaccnatctcngc 960

Db	901	AAANNTNANGANNANNNNTNNAANNNNANCATGGAANGAATTAACCNATNTCNGC	960
Qy	961	ngntnctntntnaatccnttgaagtngtntangcnggtgncntcnaatnn	1020
Db	961	NGNNTCTTNTNATNAATCCNTNTGAGTNGTNTANGCNGGTGGNACNTCAATNN	1020
Qy	1021	ntnnncantngcnggnagtatgcntntcaatggnnnatgataantatgcnttnna	1080
Db	1021	NTNNGNCANTNGCGGNAGTATGCNNTNCAATGGNNATGATTAATATGCNNTTNA	1080
Qy	1081	ncatnnnatnnangntanaattntatggnttagnggttnantttannngangcnga	1140
Db	1081	NCATNNATNNANGTANAATTTTATGGNTTAGNGGTNANTTTANNANGANGCNGA	1140
Qy	1141	agatngngtntntnaantnaaaangntnnnatcngannntntngantantgttg	1200
Db	1141	AGATGNGGNGTNTNAAATTTAAAANGGTNNNATCGANNNTNTNGANTANGTTGG	1200
Qy	1201	ngantntntaaacnataanaacnctntannnnnnntatannncantnaaaaannt	1260
Db	1201	NGANTTNTTAAACCNATNAANAACCNCTWTANNNNNNNTTATNNNCANTNAAAAAANT	1260
Qy	1261	nnannnnnnnnntannnaannnnnnnnnnnnnnnnnnnnnnatgaaattacaga	1320
Db	1261	NNANNNNNNNNNTANNNAANNNNNNNNNNNNNNNNNNNNNNATGAAATTTACAGA	1320
Qy	1321	gttaannn	1328
Db	1321	GTTAAANN	1328

RESULT	2
A97468	
LOCUS	A97468
DEFINITION	Sequence 24 from Patent WO9916780.
ACCESSION	A97468
VERSION	A97468.1 GI:5780814
KEYWORDS	.
SOURCE	unidentified.
ORGANISM	unidentified unclassified.
REFERENCE	1 (bases 1 to 44)
AUTHORS	Gala,J. and Vannuffel,P.
TITLE	GENETIC SEQUENCES, DIAGNOSTIC AND/OR QUANTIFICATION METHODS AND DEVICES FOR THE IDENTIFICATION OF STAPHYLOCOCCI STRAINS
JOURNAL	Patent: WO 9916780-A 24 08-APR-1999;
FEATURES	GALA JEAN LJC (BE); UNIV LOUVAIN (BE) Location/Qualifiers 1..44 /organism="unidentified" /db_xref="taxon:32644"
BASE COUNT	13 a 1 c 9 g 8 t
ORIGIN	13 others

RESULT	3	
A97454		
LOCUS	A97454	43 bp DNA
DEFINITION	Sequence 10 from Patent WO9916780.	linear
ACCESSION	A97454	
VERSION	A97454.1	GI:6780800
KEYWORDS	.	
SOURCE	unidentified.	

ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 43)
AUTHORS Gala,J. and Vannuffel, P.
TITLE GENETIC SEQUENCES, DIAGNOSTIC AND/OR QUANTIFICATION METHODS AND
DEVICES FOR THE IDENTIFICATION OF STAPHYLOCOCCI STRAINS
JOURNAL Patent: WO 9216780-A 10 08-APR-1999;
GALA JEAN LUC (BE); UNIV LOUVAIN (BE)
FEATURES
 source
 Location/Qualifiers
 1. .43
 /organism="unidentified"
 /db_xref="taxon:32644"
BASE COUNT 19 a 1 c 7 g 4 t 12 others
ORIGIN

Query Match 3.2%; Score 43; DB 6; Length 43;
Best Local Similarity 100.0%; Pred. NO. 1.3e-17;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 552 gnaannnaacnaaaaaagctnnnaanaaatgngttnaaagt 594
Db 1 GNAANNNAACNAAAAAAGCTNNNAANAATGNGTNAAGT 43

RESULT	4
A97457	
LOCUS	linear
DEFINITION	Sequence 13 from Patent WO9916780.
ACCESSION	A97457
VERSION	A97457.1 GI:6780803
KEYWORDS	.
SOURCE	unidentified.
ORGANISM	unidentified unclassified
REFERENCE	1 (bases 1 to 40)
AUTHORS	Gala,J.C and Vannuffel,P.
TITLE	GENETIC SEQUENCES, DIAGNOSTIC AND/OR QUANTIFICATION METHODS AND DEVICES FOR THE IDENTIFICATION OF STAPHYLOCOCCI STRAINS
JOURNAL	Patent: WO 9916780-A 13 08-APR-1999;
FEATURES	GALA JEAN LUC (BE); UNIV LOUVAIN (BE) Location/Qualifiers l..40 /organism="unidentified" /db_xref="taxon:32644"
source	
BASE COUNT	10 a 4 c 6 g 9 t 11 others
ORIGIN	

[illegible]

FEATURES GALA JEAN LUC (BE); UNIV LOUVAIN (BE)
source Location/Qualifiers
1. .37
/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 13 a 1 c 6 g 7 t 10 others
ORIGIN

Query Match 2.8%; Score 37; DB 6; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.5e-13;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 141 tagtngnataaanaanaanaangangnangnattgc 177
|||||
Db 1 TAGTNGNATNANANANANATNANGANGNATTGTC 37

RESULT 6
A97446 35 bp DNA linear PAT 26-JAN-2000
LOCUS A97446
DEFINITION Sequence 2 from Patent WO9916780.
ACCESSION A97446
VERSION A97446.1 GI:6780792
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 35)
AUTHORS Gala,J. and Vannuffel,P.
TITLE GENETIC SEQUENCES, DIAGNOSTIC AND/OR QUANTIFICATION METHODS AND DEVICES FOR THE IDENTIFICATION OF STAPHYLOCOCCI STRAINS
JOURNAL Patent: WO 9916780-A 2 08-APR-1999;
GALA JEAN LUC (BE); UNIV LOUVAIN (BE)
FEATURES Location/Qualifiers
source 1. .35
/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 12 a 3 c 3 g 9 t 8 others
ORIGIN

Query Match 2.6%; Score 35; DB 6; Length 35;
Best Local Similarity 100.0%; Pred. No. 3.4e-12;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 anaatgaantttacnaatttncngcnaagant 48
|||||
Db 1 ANAATGAANTTTACNAAATTTCNCGNANAGANTT 35

RESULT 7
A97452 35 bp DNA linear PAT 26-JAN-2000
LOCUS A97452
DEFINITION Sequence 8 from Patent WO9916780.
ACCESSION A97452
VERSION A97452.1 GI:6780798
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 35)
AUTHORS Gala,J. and Vannuffel,P.
TITLE GENETIC SEQUENCES, DIAGNOSTIC AND/OR QUANTIFICATION METHODS AND DEVICES FOR THE IDENTIFICATION OF STAPHYLOCOCCI STRAINS
JOURNAL Patent: WO 9916780-A 8 08-APR-1999;
GALA JEAN LUC (BE); UNIV LOUVAIN (BE)
FEATURES Location/Qualifiers
source 1. .35
/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 8 a 3 c 3 g 13 t 8 others
ORIGIN

Query Match 2.6%; Score 35; DB 6; Length 35;
Best Local Similarity 100.0%; Pred. No. 3.4e-12;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 197 gtncngnatgaanaantttanaantatttattc 231
|||||
Db 1 GTNCNGNATGAANAANTTTNANANTATTATTATTC 35

RESULT 8
A97467 35 bp DNA linear PAT 26-JAN-2000
LOCUS A97467
DEFINITION Sequence 23 from Patent WO9916780.
ACCESSION A97467
VERSION A97467.1 GI:6780813
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 35)
AUTHORS Gala,J. and Vannuffel,P.
TITLE GENETIC SEQUENCES, DIAGNOSTIC AND/OR QUANTIFICATION METHODS AND DEVICES FOR THE IDENTIFICATION OF STAPHYLOCOCCI STRAINS
JOURNAL Patent: WO 9916780-A 23 08-APR-1999;
GALA JEAN LUC (BE); UNIV LOUVAIN (BE)
FEATURES Location/Qualifiers
source 1. .35
/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 9 a 3 c 6 g 9 t 8 others
ORIGIN

Query Match 2.6%; Score 35; DB 6; Length 35;
Best Local Similarity 100.0%; Pred. No. 3.4e-12;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1040 agntatgcnttncatgaggnatgatttaattatgc 1074
|||||
Db 1 AGNTATGCNNTNCATGAGGNATGATTTAATTATGTC 35

RESULT 9
A97459 32 bp DNA linear PAT 26-JAN-2000
LOCUS A97459
DEFINITION Sequence 15 from Patent WO9916780.
ACCESSION A97459
VERSION A97459.1 GI:6780805
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 32)
AUTHORS Gala,J. and Vannuffel,P.
TITLE GENETIC SEQUENCES, DIAGNOSTIC AND/OR QUANTIFICATION METHODS AND DEVICES FOR THE IDENTIFICATION OF STAPHYLOCOCCI STRAINS
JOURNAL Patent: WO 9916780-A 15 08-APR-1999;
GALA JEAN LUC (BE); UNIV LOUVAIN (BE)
FEATURES Location/Qualifiers
source 1. .32
/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 16 a 2 c 4 g 1 t 9 others
ORIGIN

Query Match 2.4%; Score 32; DB 6; Length 32;
Best Local Similarity 100.0%; Pred. No. 3.7e-10;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 818 aanganatnganaaangncnganaaaaaa 849

```

Db 1 AANGANATNGAANAANGCNGAANAANAAAA 32
|||||
RESULT 10
LOCUS A97466
DEFINITION Sequence 22 from Patent WO9916780.
ACCESSION A97466
VERSION A97466.1 GI:6780812
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
BASE COUNT 6 a 3 c 8 g 8 t 7 others
ORIGIN

Query Match 2.4%; Score 32; DB 6; Length 32;
Best Local Similarity 100.0%; Pred. No. 3.7e-10;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 977 aatccntntgaagtngtnttantangcnggtgg 1008
|||||
Db 1 AATCCNTNTGAAGTNGTNTANTANGCNGGTGG 32
|||||

RESULT 11
LOCUS A97449
DEFINITION Sequence 5 from Patent WO9916780.
ACCESSION A97449
VERSION A97449.1 GI:6780795
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
BASE COUNT 7 a 4 c 2 g 4 t 8 others
ORIGIN

Query Match 1.9%; Score 25; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 atgncnnnagncatttnacncana 92
|||||
Db 1 ATGNCNNANAGNCATTTNACNCANA 25
|||||

RESULT 12
AC107183/c
LOCUS

```

```

DEFINITION Rattus norvegicus clone CH230-121F14, *** SEQUENCING IN PROGRESS
***, 9 unordered pieces.
AC107183
VERSION AC107183.1 GI:18158341
KEYWORDS HTG: HTGS_PHASE1.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 13139)
AUTHORS Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbarella,J.,
Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J.,
Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C.,
Burck,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F.,
Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R.,
Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C.,
Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C.,
Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O.,
Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H.,
Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C.,
Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J.,
Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T.,
Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S.,
Hamilton,K., Harris,C., Harris,K., Hart,M., Guevara,W., Gunaratne,P., Hale,S.,
Hernandez,J., Hernandez,O., Hodgson,A., Hogue,M., Holloway,C.,
Hollins,B., Homs,F., Howard,S., Huber,J., Hulyk,S., Hume,J.,
Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S.,
Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J.,
Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C.,
Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W.,
Louiseged,H., Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R.,
Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A.,
Martinez,E., Massey,E., Mawhiney,E., McLeod,M.P., Meador,M.,
Mei,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K.,
Morgan,A., Morris,S., Moser,M., Neal,D., Newton,J., Newton,N.,
Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokenkwo,S.,
Ogulu,M., Okwunnu,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B.,
Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L.,
Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojubokan,I., Rolfe,M.,
Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shoostari,N.,
Sisson,I., Sodergren,E., Sonaika,T., Sparks,A., Stanley,H.,
Stonson,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K.,
Tang,H., Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N.,
Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalón,D., Vinson,R.,
Wall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C.,
Watlington,S., Williams,G., Williamson,A., Wleczyk,R., Wooden,S.,
Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G. and Gibbs,R.
Direct Submission
Unpublished
2 (bases 1 to 13139)
Worley,K.C.
Direct Submission
Submitted (16-JAN-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GPGP
Center clone name: CH230-121F14
----- Summary Statistics
Sequencing vector: Plasmid; M7789
Chemistry: Dye-terminator Big Dye; 97% of reads
Assembly program: Phrap; version 0.990329First call to
findphrapList
Consensus quality: 10722 bases at least Q40
Consensus quality: 12181 bases at least Q30

```

Consensus quality: 13502 bases at least Q20
 Estimated insert size: 9083; sum-of-contrigs estimation
 Quality coverage: 0x in Q20 bases; agarose-1p estimation
 Quality coverage: 0.1x in Q20 bases; sum-of-contrigs estimation

* NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hgsc.bcm.tmc.edu/docs/genbank/draft_data.html).
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 9 contrigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contrigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1 1384: contrig of 1384 bp in length
 * 1385 1484: gap of unknown length
 * 1485 3017: contrig of 1533 bp in length
 * 3018 3117: gap of unknown length
 * 3118 4473: contrig of 1356 bp in length
 * 4474 4573: gap of unknown length
 * 4574 5627: contrig of 1054 bp in length
 * 5628 5727: gap of unknown length
 * 5728 7171: contrig of 1444 bp in length
 * 7172 7271: gap of unknown length
 * 7272 8548: contrig of 1277 bp in length
 * 8549 10197: gap of unknown length
 * 10198 10287: gap of unknown length
 * 10298 11848: contrig of 1551 bp in length
 * 11849 11948: gap of unknown length
 * 11949 13139: contrig of 1191 bp in length.

FEATURES
 source 1. 13139
 /organism="Rattus norvegicus"
 /db_xref="taxon:10116"
 /clone="CH230-121F14"

BASE COUNT 3570 a 2577 c 2844 g 3232 t 916 others
 ORIGIN

Query Match 1.9%; Score 25; DB 2; Length 13139;
 Best Local Similarity 100.0%; Pred. No. 3.7e-06;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1282 aaaaaaaaaaaaaaaaaaaaaa 1306
 Db 4331 aaaaaaaaaaaaaaaaaaaaaa 4307

RESULT 13
 AC108260 59240 bp DNA linear HTG 27-JAN-2002
 LOCUS Rattus norvegicus clone CH230-190K14, *** SEQUENCING IN PROGRESS
 DEFINITION *** 46 unordered pieces.
 AC108260
 VERSION AC108260.1 GI:18377040
 KEYWORDS HTG; HTGS_PHASE1.
 SOURCE Norway rat.
 ORGANISM Rattus norvegicus
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 59240)

REFERENCE
 AUTHORS Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
 Alshrocks,S.L., Amarantunge,H.C., Are,J.R., Ayele,M., Banks,T.,
 Barbatis,J., Benton,J., Blmage,K., Blankenburg,K., Bonnin,D.,
 Bouck,J., Bowls,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,
 Buhaq,C., Burck,P., Burkett,C., Butrell,K.L., Byrd,N.C.,
 Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
 Chen,G., Chen,R., Chen,Z., Chowdhury,I., Christopoulos,C.,
 Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
 Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,

TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL

COMMENT

Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
 Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
 Earhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
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 Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
 Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
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 Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
 Weinstock,G. and Glibbs,R.
 Direct Submission
 2 (bases 1 to 59240)

Worley,K.C.
 Direct Submission
 Submitted (27-JAN-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 ----- Genome Center

Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu
 ----- Project Information
 Center project name: GM2I
 Center clone name: CH230-190K14
 ----- Summary Statistics
 Chemistry: Dye-terminator Big Dye; 99% of reads
 Assembly program: Phrap; version 0.990339first call to
 findPhraplist

Consensus quality: 32577 bases at least Q40
 Consensus quality: 36104 bases at least Q30
 Consensus quality: 38234 bases at least Q20
 Estimated insert size: 21683; sum-of-contrigs estimation
 Quality coverage: 0x in Q20 bases; agarose-1p estimation
 Quality coverage: 0.2x in Q20 bases; sum-of-contrigs estimation

* NOTE: Estimated insert size may differ from sequence length.
 * (see http://www.hgsc.bcm.tmc.edu/docs/genbank/draft_data.html).
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 46 contrigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contrigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
 * 1 896: contrig of 896 bp in length
 * 897 996: gap of unknown length
 * 997 1888: contrig of 892 bp in length
 * 1889 1989: gap of unknown length
 * 1989 2937: contrig of 949 bp in length

2366 2465: gap of unknown length
2466 3550: contig of 1085 bp in length
3551 3650: gap of unknown length
3651 5170: contig of 1520 bp in length
5171 5270: gap of unknown length
5271 6565: contig of 1295 bp in length
6566 8023: gap of unknown length
8024 8123: contig of 1358 bp in length
8124 9194: gap of unknown length
9195 9294: contig of 1071 bp in length
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11153 11252: gap of unknown length
11253 12495: contig of 1243 bp in length
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17578 18865: contig of 1289 bp in length
18866 18965: gap of unknown length
18966 20345: contig of 1380 bp in length
20346 20445: gap of unknown length
20446 21857: contig of 1412 bp in length
21858 21957: gap of unknown length
21958 24260: contig of 2303 bp in length
24261 24360: gap of unknown length
24361 25733: contig of 1373 bp in length
25734 25833: gap of unknown length
25834 27583: contig of 1750 bp in length
27584 27683: gap of unknown length
27684 29598: contig of 1915 bp in length
29599 29698: gap of unknown length
29699 32020: contig of 2322 bp in length
32021 32120: gap of unknown length
32121 34325: contig of 2205 bp in length
34326 37026: contig of 2601 bp in length
37027 37127: gap of unknown length
37128 39043: contig of 1917 bp in length
39044 39143: gap of unknown length
39144 40727: contig of 1584 bp in length
40728 42654: contig of 1827 bp in length
42655 42754: gap of unknown length
42755 45027: contig of 2273 bp in length
45028 45127: gap of unknown length
45128 47695: contig of 2568 bp in length
47696 47795: gap of unknown length
47796 50748: contig of 2953 bp in length
50749 50848: gap of unknown length
50849 52227: contig of 1379 bp in length
52228 52327: gap of unknown length
52329 54082: contig of 1755 bp in length
54083 54182: gap of unknown length
54183 57029: contig of 2847 bp in length
57030 57129: gap of unknown length
57130 60259: contig of 3130 bp in length
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60360 64505: contig of 4446 bp in length
64506 64605: gap of unknown length
64606 70056: contig of 5451 bp in length
70057 70156: gap of unknown length
70157 75954: contig of 5798 bp in length
75955 76054: gap of unknown length
76055 81464: contig of 5410 bp in length
81465 81564: gap of unknown length
81565 87781: contig of 6217 bp in length
87782 94743: contig of 6862 bp in length
94744 94843: gap of unknown length

FEATURES
source
* 94844 102209: contig of 7366 bp in length
* 102210 102309: gap of unknown length
* 102310 107145: contig of 4836 bp in length
* 107146 107245: gap of unknown length
* 107246 114459: contig of 7214 bp in length
* 114460 114559: gap of unknown length
* 114560 122927: contig of 8368 bp in length
* 122928 124083: contig of 1056 bp in length.
* 123028 Location/Qualifiers
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/db_xref="taxon:9606"
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/clone="CTD-2192H8"
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Query Match 1.9% Score 25; DB 2; Length 124083;
 Best Local Similarity 100.0%; Pred. No. 2e-06;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1283 nnnnnnnnnnnnnnnnnnnnnna 1307
 |||||nnnnnnnnnnnnnnnnnnnnnnnn
 Db 4884 NNNNNNNNNNNNNNNNNNNNA 4908

RESULT 15

AC098325/c

LOCUS

DEFINITION

Rattus norvegicus clone CH230-1M6, ** SEQUENCING IN PROGRESS ***,

18 unordered pieces.

AC098325

AC098325.1 GI:16328092

HTG: HTGS_PHASE1.

Norway rat.

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

1 (bases 1 to 50132)

Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-Osman,F.R., Allen,C.,

Albrooks,S.L., Amarantunge,H.C., Are,J.R., Banks,T., Barbara,J.,

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Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C.,

Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F.,

Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R.,

Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C.,

Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C.,

Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O.,

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Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A.,

Martinez,E., Massey,E., Mawhiney,E., McLeod,M.P., Meador,M.,

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Morgan,M., Morris,S., Moser,M., Neal,D., Newton,J., Newton,N.,

Nguyen,A., Nguyen,S., Nguyen,N., Nickerson,E., Nwokenkwo,S.,

Ogah,M., Okwunonu,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B.,

Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L.,

Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojibokan,I., Rolfe,M.,

Ruiz,S., Savary,G., Scherer,S., Scott,G., Shen,H., Shoohtari,N.,

Sisson,I., Sodergren,E., Sonaike,T., Sparks,A., Stanley,H.,

Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K.,

Tang,H., Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N.,

Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalobos,D., Vinson,R.,

Wall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C.,
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 Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
 Weinstein,G., and Gibbs,R.

Direct Submission

Unpublished

2 (bases 1 to 50132)

Worley,K.C.

Direct Submission

Submitted (23-OCT-2001) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA

COMMENT

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: http://www.hgsc.bcm.tmc.edu/

Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: TUKX

Center clone name: CH230-1M6

----- Summary Statistics

Assembly program: Phrap; version 0.990329

Consensus quality: 30546 bases at least Q40

Consensus quality: 36166 bases at least Q30

Consensus quality: 40318 bases at least Q20

Estimated insert size: 92905; sum-of-contigs estimation

Quality coverage: 0x in Q20 bases; agarose-fp estimation

Quality coverage: 0.9x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
 (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
 * NOTE: This is a 'working draft' sequence. It currently
 consists of 18 contigs. The true order of the pieces
 is not known and their order in this sequence record is
 arbitrary. Gaps between the contigs are represented as
 runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 as soon as it is available and the accession number will
 be preserved.

1 4238: contig of 4238 bp in length
 4239 4338: gap of unknown length
 4339 7327: contig of 2989 bp in length
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 7428 9490: contig of 2062 bp in length
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 32969 36027: contig of 3058 bp in length
 36027 38452: contig of 2326 bp in length
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 38553 40781: contig of 2229 bp in length
 40782 40881: gap of unknown length
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 42951 43050: gap of unknown length
 43051 45544: contig of 2494 bp in length
 45545 45645: gap of unknown length
 45645 47950: contig of 2306 bp in length
 47951 48050: gap of unknown length

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 22, 2002, 05:51:01 ; Search time 241.5 Seconds
(without alignments)
9441.252 Million cell updates/sec

Title: us-09-509-234c-1
Perfect score: 1328
Sequence: 1 nnnnnnnnnnnnaatga.....gaaattacagagttaannn 1328

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1736436 seqs, 858457221 residues

Word size : 15

Total number of hits satisfying chosen parameters: 454

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : N.Geneseq_032802.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	1328	100.0	1328	20	AA337797 Staphylococcus sp.
2	44	3.3	44	20	AA337773 Staphylococcus sp.
3	43	3.2	43	20	AA337759 Staphylococcus sp.
4	40	3.0	40	20	AA337762 Staphylococcus sp.
5	37	2.8	37	20	AA337756 Staphylococcus sp.
6	35	2.6	35	20	AA337772 Staphylococcus sp.
7	35	2.6	35	20	AA337757 Staphylococcus sp.
8	35	2.6	35	20	AA337751 Staphylococcus sp.
9	32	2.4	32	20	AA337764 Staphylococcus sp.

Staphylococcus sp.
Staphylococcus sp.
Human polynucleoti
Human gene express
Stealth virus plas
Stealth virus nucl
Human neuroblastom
Staphylococcus sp.
Human polynucleoti
Human colon cancer
Human neuroblastom
Staphylococcus sp.
Staphylococcus sp.
EST clone CJ420
Staphylococcus sp.
Human colon cancer
Human colon cancer
Aspergillus oryzae
Staphylococcus aur
Staphylococcus epi
S. epidermidis ope
Staphylococcus aur
Staphylococcus aur
Staphylococcus aur
Staphylococcus cap
Staphylococcus sci
Staphylococcus xyl
Staphylococcus sch
Staphylococcus hae
S. epidermidis gen
Staphylococcus aur
Staphylococcus sp.
Staphylococcus sp.
Human polynucleoti
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Human polynucleoti
Staphylococcus aur
Staphylococcus aur
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Human polynucleoti
Human polynucleoti
Human polynucleoti
Aspergillus oryzae
Staphylococcus aur
Human colon cancer
Human colon cancer
Human gene express
Human gene express
Human gene express
Human neuroblastom
Human gene express
Human validated ca
Human gene express
Human gene express
Human gene express
Human gene express
Human validated ca
Human neuroblastom
Human gene express
Proliferative glom
Human colon cancer
Human colon cancer
Aspergillus oryzae
Aspergillus oryzae
Aspergillus oryzae
Human colon cancer
Aspergillus oryzae
Staphylococcus lug
Staphylococcus aur

83	17	1.3	2067	22	AAS56381	Human cDNA for an
C 84	17	1.3	7900	18	AAV74449	Staphylococcus aur
C 85	17	1.3	10322	18	AAV74409	Staphylococcus aur
C 86	16	1.2	222	6	AAN50757	Sequence of the hu
C 87	16	1.2	268	21	AAA01235	Human colon cancer
C 88	16	1.2	287	22	AAI11577	Human breast cancer
C 89	16	1.2	293	20	AAK98663	Human cancer cell
C 90	16	1.2	298	22	AAI84740	Human polynucleoti
C 91	16	1.2	301	22	AAH73288	Human cervical can
C 92	16	1.2	323	18	AAV78716	Staphylococcus aur
C 93	16	1.2	325	22	AAI84998	Human polynucleoti
C 94	16	1.2	336	22	AAI88676	Human polynucleoti
C 95	16	1.2	345	22	AAI80690	Human polynucleoti
C 96	16	1.2	350	22	AAI81061	Novel human diagno
C 97	16	1.2	353	22	AAS36985	B2HFLS20W cDNA 11b
C 98	16	1.2	357	22	AAI31351	cDNA encoding a hu
C 99	16	1.2	358	20	AAZ30048	Sequence from Flgu
C 100	16	1.2	359	20	AAK27759	Human polynucleoti
C 101	16	1.2	363	22	AAI84982	Sequence from Flgu
C 102	16	1.2	364	20	AAK27761	Human cancer relat
C 103	16	1.2	369	22	AAS59176	Human polynucleoti
C 104	16	1.2	374	22	AAI91055	Human polynucleoti
C 105	16	1.2	377	21	AAI14255	Aspergillus oryzae
C 106	16	1.2	382	22	AAI65303	Novel human polynu
C 107	16	1.2	383	22	AAI64663	Novel human polynu
C 108	16	1.2	391	22	AAI17399	Human bone marrow
C 109	16	1.2	397	23	AAS82692	DNA encoding novel
C 110	16	1.2	399	22	AAI89674	Human polynucleoti
C 111	16	1.2	399	22	AAI89674	Human polynucleoti
C 112	16	1.2	399	22	AAI89674	Human polynucleoti
C 113	16	1.2	399	22	AAI89674	Human polynucleoti
C 114	16	1.2	407	22	AAS56404	DNA encoding novel
C 115	16	1.2	407	22	AAI81706	Human cDNA for an
C 116	16	1.2	408	23	AAS80379	DNA encoding novel
C 117	16	1.2	408	23	AAS8052	DNA encoding novel
C 118	16	1.2	410	23	AAI86512	Human polynucleoti
C 119	16	1.2	411	23	AAI86512	DNA encoding novel
C 120	16	1.2	413	22	AAI09111	Human breast cance
C 121	16	1.2	414	22	AAI85302	Human polynucleoti
C 122	16	1.2	417	23	AAI67412	DNA encoding novel
C 123	16	1.2	418	22	AAI93345	Human polynucleoti
C 124	16	1.2	419	23	AAI57637	DNA encoding novel
C 125	16	1.2	420	22	AAI87376	Human polynucleoti
C 126	16	1.2	433	22	AAI80776	Human polynucleoti
C 127	16	1.2	436	22	AAI80539	Human polynucleoti
C 128	16	1.2	441	23	AAI83978	DNA encoding novel
C 129	16	1.2	441	23	AAI88169	DNA encoding novel
C 130	16	1.2	444	23	AAI891551	DNA encoding novel
C 131	16	1.2	447	22	AAI82415	Human polynucleoti
C 132	16	1.2	453	22	AAI81970	Human polynucleoti
C 133	16	1.2	468	23	AAI69012	DNA encoding novel
C 134	16	1.2	468	23	AAI69012	DNA encoding novel
C 135	16	1.2	468	23	AAI69012	DNA encoding novel
C 136	16	1.2	468	23	AAI69012	DNA encoding novel
C 137	16	1.2	482	20	AAK27756	Promoter for T7 RN
C 138	16	1.2	482	20	AAK27756	Promoter for T7 RN
C 139	16	1.2	486	21	AAI14726	Aspergillus oryzae
C 140	16	1.2	488	22	AAI11444	Human breast cance
C 141	16	1.2	488	22	AAI88888	Human polynucleoti
C 142	16	1.2	517	22	AAI85113	Human polynucleoti
C 143	16	1.2	517	22	AAI85113	Human polynucleoti
C 144	16	1.2	524	21	AAI87395	Human prostate can
C 145	16	1.2	535	21	AAI52310	HSPH-1 partial cDN
C 146	16	1.2	626	21	AAI14232	Aspergillus oryzae
C 147	16	1.2	626	21	AAI14232	Aspergillus oryzae
C 148	16	1.2	654	18	AAI3442	Staphylococcus aur
C 149	16	1.2	659	21	AAI12045	Aspergillus oryzae
C 150	16	1.2	669	21	AAI14156	Aspergillus oryzae
C 151	16	1.2	669	21	AAI15000	Human neuroblastom
C 152	16	1.2	682	21	AAI2045	Human colon cancer
C 153	16	1.2	688	21	AAI14199	Aspergillus oryzae
C 154	16	1.2	700	22	AAI86748	Human polynucleoti
C 155	16	1.2	705	21	AAI01914	Human colon cancer
C 156	16	1.2	705	21	AAI01914	Human colon cancer
C 157	16	1.2	708	21	AAI11887	Aspergillus oryzae
C 158	16	1.2	708	21	AAI11887	Aspergillus oryzae
C 159	16	1.2	710	20	AAI15426	Human gene express
C 160	16	1.2	711	20	AAI12785	Aspergillus oryzae
C 161	16	1.2	713	20	AAI01958	Human colon cancer
C 162	16	1.2	716	20	AAI215279	Human gene express
C 163	16	1.2	716	20	AAI215253	Human gene express
C 164	16	1.2	716	22	AAI96667	Human neuroblastom
C 165	16	1.2	717	21	AAI3971	Aspergillus oryzae
C 166	16	1.2	717	21	AAI3971	Human gene express
C 167	16	1.2	719	20	AAI215240	Aspergillus oryzae
C 168	16	1.2	725	21	AAI14386	Aspergillus oryzae
C 169	16	1.2	726	21	AAI14617	Human gene express
C 170	16	1.2	728	20	AAI215157	Human neuroblastom
C 171	16	1.2	733	22	AAI97046	Human colon cancer
C 172	16	1.2	734	21	AAI01782	Human polynucleoti
C 173	16	1.2	735	22	AAI97605	Human polynucleoti
C 174	16	1.2	736	21	AAI02413	Arabidopsis thalia
C 175	16	1.2	744	22	AAI03845	Human polynucleoti
C 176	16	1.2	744	22	AAI03845	Human colon cancer
C 177	16	1.2	745	21	AAI01747	Human colon cancer
C 178	16	1.2	745	21	AAI01747	Human colon cancer
C 179	16	1.2	752	21	AAI15164	Human gene express
C 180	16	1.2	752	21	AAI15164	Human gene express
C 181	16	1.2	764	22	AAI95741	Human gene express
C 182	16	1.2	764	22	AAI95741	Human gene express
C 183	16	1.2	772	22	AAI94437	Human gene express
C 184	16	1.2	772	22	AAI94437	Human gene express
C 185	16	1.2	776	20	AAI16561	Human gene express
C 186	16	1.2	776	20	AAI98743	Human gene express
C 187	16	1.2	789	20	AAI16082	Human gene express
C 188	16	1.2	791	20	AAI15500	Human gene express
C 189	16	1.2	799	20	AAI16599	Human gene express
C 190	16	1.2	807	20	AAI16599	Human gene express
C 191	16	1.2	819	20	AAI16751	Human gene express
C 192	16	1.2	834	20	AAI21645	Human gene express
C 193	16	1.2	834	20	AAI21645	Human gene express
C 194	16	1.2	839	21	AAI96966	Human gene express
C 195	16	1.2	847	20	AAI21648	Human gene express
C 196	16	1.2	864	20	AAI21648	Human gene express
C 197	16	1.2	867	21	AAI02283	Human gene express
C 198	16	1.2	889	22	AAI94373	Human gene express
C 199	16	1.2	900	21	AAI14572	Human gene express
C 200	16	1.2	918	21	AAI02305	Human gene express
C 201	16	1.2	925	21	AAI02110	Cat flea hindgut a
C 202	16	1.2	929	21	AAI02110	Proliferative gliom
C 203	16	1.2	933	22	AAI77026	Human colon cancer
C 204	16	1.2	950	21	AAI02120	Aspergillus oryzae
C 205	16	1.2	952	22	AAI77037	Human colon cancer
C 206	16	1.2	953	20	AAI99064	Human gene express
C 207	16	1.2	961	20	AAI215195	Myobacterium tube
C 208	16	1.2	963	22	AAI31612	Human gene express
C 209	16	1.2	985	22	AAI21016	Human gene express
C 210	16	1.2	999	20	AAI217304	Human gene express
C 211	16	1.2	1005	21	AAI02074	Human colon cancer
C 212	16	1.2	1005	21	AAI02074	Human colon cancer
C 213	16	1.2	1021	24	AAI99215	Mouse ischaemic co
C 214	16	1.2	1024	21	AAI97188	Human colon cancer
C 215	16	1.2	1078	21	AAI01684	Human gene express
C 216	16	1.2	1095	20	AAI16986	Borrelia burgdorfe
C 217	16	1.2	1100	21	AAI50124	Human validated ca
C 218	16	1.2	1122	20	AAI98750	Human colon cancer
C 219	16	1.2	1156	21	AAI02530	Human colon cancer
C 220	16	1.2	1178	21	AAI02530	Human colon cancer
C 221	16	1.2	1186	21	AAI02489	Human colon cancer
C 222	16	1.2	1230	21	AAI01790	Human gene express
C 223	16	1.2	1243	22	AAI89503	Human gene express
C 224	16	1.2	1274	20	AAI16994	DNA encoding novel
C 225	16	1.2	1279	23	AAI90540	Human colon cancer
C 226	16	1.2	1315	21	AAI02116	Human gene express
C 227	16	1.2	1315	20	AAI17173	Human gene express
C 228	16	1.2	1315	20	AAI17173	Human gene express

c 375	15	1.1	970	21	AAA02167	Human colon cancer
c 376	15	1.1	980	18	AA801819	Hammerhead ribozym
c 377	15	1.1	991	21	AAA02076	Human colon cancer
c 378	15	1.1	1024	21	AAZ57183	Human prostate can
c 379	15	1.1	1024	21	AAZ57188	Human prostate can
c 380	15	1.1	1036	21	AAA02095	Human colon cancer
c 381	15	1.1	1060	21	AAA02582	Human colon cancer
c 382	15	1.1	1060	21	AAA02582	Human colon cancer
c 383	15	1.1	1082	21	AAA02370	Human colon cancer
c 384	15	1.1	1103	20	AAZ17554	Human gene expres
c 385	15	1.1	1123	22	AAI17669	Human neuroblastom
c 386	15	1.1	1178	21	AAA02530	Human colon cancer
c 387	15	1.1	1196	21	AAA02459	Human colon cancer
c 388	15	1.1	1209	21	AAA02464	Human colon cancer
c 389	15	1.1	1230	21	AAA01790	Human colon cancer
c 390	15	1.1	1273	20	AAZ17014	Human gene expres
c 391	15	1.1	1274	22	AAI15253	Human polynucleoti
c 392	15	1.1	1275	22	AAZ53132	DNA encoding novel
c 393	15	1.1	1328	20	AAZ53717	Staphylococcus sp.
c 394	15	1.1	1373	21	AAA01835	Human colon cancer
c 395	15	1.1	1462	22	AAZ56397	Human CDNA for an
c 396	15	1.1	1472	18	AAZ74984	Staphylococcus aur
c 397	15	1.1	1481	21	AAA02601	Human colon cancer
c 398	15	1.1	1498	21	AAA02082	Human colon cancer
c 399	15	1.1	1498	21	AAA02082	Human colon cancer
c 400	15	1.1	1505	20	AAZ17177	Human gene express
c 401	15	1.1	1601	22	AAZ56538	Human CDNA for an
c 402	15	1.1	1604	22	AAZ56543	Human CDNA for an
c 403	15	1.1	1624	22	AAI92583	Human polynucleoti
c 404	15	1.1	1633	22	AAZ56386	Human CDNA for an
c 405	15	1.1	1633	15	AAO58330	GGF2BPp5. Bos tau
c 406	15	1.1	1633	15	AAO62839	GGF2BPp5. Bos tau
c 407	15	1.1	1686	21	AAZ56646	Human secreted pro
c 408	15	1.1	2039	22	AAZ566416	Human CDNA for an
c 409	15	1.1	2039	22	AAZ566416	Human CDNA for an
c 410	15	1.1	2044	21	AAZ43874	Murine NMX3 CDNA.
c 411	15	1.1	2241	22	AAI18172	Human CDNA sequenc
c 412	15	1.1	3005	22	AAI160085	Human polynucleoti
c 413	15	1.1	3044	20	AAZ81115	Seneescence-associa
c 414	15	1.1	3086	23	AAZ05296	Drosophila melanog
c 415	15	1.1	3106	22	AAH72702	Human cervical can
c 416	15	1.1	3316	23	AAI10742	Drosophila melanog
c 417	15	1.1	3470	20	AAZ92070	Human muscarinic a
c 418	15	1.1	3787	18	AAZ74686	Staphylococcus aur
c 419	15	1.1	4145	23	AAI13468	Drosophila melanog
c 420	15	1.1	4245	18	AAZ80506	Cell proliferation
c 421	15	1.1	4549	22	AAZ74485	Staphylococcus aur
c 422	15	1.1	4826	18	AAZ74586	Staphylococcus aur
c 423	15	1.1	5602	18	AAZ74440	Staphylococcus aur
c 424	15	1.1	6810	20	AAZ0267	Borrelia burgdorfe
c 425	15	1.1	8668	14	AAO50433	Partial human geno
c 426	15	1.1	9834	18	AAZ74348	Staphylococcus aur
c 427	15	1.1	11050	18	AAZ74407	Staphylococcus aur
c 428	15	1.1	11802	18	AAZ74381	Staphylococcus aur
c 429	15	1.1	22977	22	AAZ77150	Human immune/haema
c 430	15	1.1	24025	17	AAI17455	Mutated BRCA1 geno
c 431	15	1.1	24025	17	AAI17515	Mutated BRCA1 geno
c 432	15	1.1	24026	17	AAI152612	BRCA1, human breas
c 433	15	1.1	24026	17	AAI17512	Mutated BRCA1 geno
c 434	15	1.1	24026	17	AAI17513	Mutated BRCA1 geno
c 435	15	1.1	24026	17	AAI17514	Mutated BRCA1 geno
c 436	15	1.1	24026	17	AAI17516	Mutated BRCA1 geno
c 437	15	1.1				

448	1.5	24026	17	AAAT17530	BRCA1 genomic sequ
449	1.5	24026	17	AAAT18325	BRCA1, human breast
450	1.5	24029	17	AAAT17520	Mutated BRCA1 geno
451	1.5	24031	17	AAAT17525	Mutated BRCA1 geno
452	1.5	29555	18	AAV74517	Staphylococcus aur
453	1.5	30246	18	AAV74367	Staphylococcus aur
454	1.1	125910	21	AAAC64370	Human KCON3 (KCNQ3

ALIGNMENTS

	RESULT	1
ID	AAK37797	standard; DNA; 1328 BP.
XX	AAK37797	
AC	AAK37797:	
DT	09-JUL-1999	(first entry)
XX		
DE	Staphylococcus sp. Fema consensus DNA sequence.	
XX		
KW	Fema; identification; detection; therapy; infection; femB;	
XX	amplification; genotyping; gram-positive bacteria; vaccine; ss.	
OS	Synthetic.	
XX	Staphylococcus sp.	
PN	W09916780-A2.	
XX		
PD	08-APR-1999.	
XX		
PF	28-SEP-1998; 98WO-BE00141.	
XX		
PR	26-SEP-1997; 97EP-0870146.	
PA	(BENA-) BELGIAN MIN NAT DEFENCE.	
PA	(UYLO-) UNIV CATHOLIQUE LOUVAIN.	
PI	Gala J, Vannuffel P;	
DR	WP1; 1999-287521/24.	
XX		
XX	New Staphylococcus-specific oligonucleotides	
PS	Claim 1; Fig 3; 48bp; English.	
CC	This invention describes novel Staphylococcus-specific oligonucleotides	
CC	based on the consensus fema nucleotide sequence which are used to	
CC	develop products for the identification, detection and therapy of	
CC	infections. The oligonucleotides can be used for the genetic	
CC	amplification, the identification and/or quantification of various fema	
CC	sequences which are specific to known or unknown Staphylococci species.	
CC	Since the fema sequence is similar to the femB sequence, the	
CC	oligonucleotides can also be used for the molecular genotyping of femB	
CC	genes of different Staphylococci species or other gram-positive bacteria.	
CC	The fema nucleic acids can also be used in therapeutic applications.	
CC	They can also be used to identify inhibitors, e.g. antibodies or	
CC	antisense oligonucleotides, for blocking expression of the fema	
CC	nucleotide sequences. They can also be used for producing vaccines	
CC	against Staphylococci infections. This sequence represents a FemA	
CC	consensus DNA sequence composed from Staphylococcus sp. sequences.	
SO	Sequence 1328 BP; 304 A; 78 C; 146 G; 227 T; 573 other;	
Query Match	100.0%; Score 1328; DB 20; Length 1328;	
Best Local Similarity	100.0%; Pred. No. 0;	
Matches 1328; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
0Y	1 nnnnnnnnnnnnaatgaatttaacaaatttnaacngcnaganttngnmmnttac 60	
db	1 nnnnnnnnnnnnaaatgaatttaacaaatttnaacngcnaganttngnmmnttac 60	

QY 1124 ttanngangcngagatgngngtntnaantnaaaaa 1167
 |||||||||||||||||||||||||||||||||||||||
 DB 1 ttanngangcngagatgngngtntnaantnaaaaa 44

RESULT 3

AA37759
 ID AAX37759 standard; DNA; 43 BP.

AC AAX37759;

DT 09-JUL-1999 (first entry)

DE Staphylococcus sp. detecting oligonucleotide 6.

KW FemA; primer; identification: detection; therapy: infection; femB;
 amplification; genotyping; gram-positive bacteria; vaccine; ss.

OS Synthetic.

XX Staphylococcus sp.

PN W09916780-A2.

PD 08-APR-1999.

PF 28-SEP-1998; 98MO-BE00141.

PR 26-SEP-1997; 97EP-0870146.

PA (BENA-) BELGIAN MIN NAT DEFENCE.
 (UYLO-) UNIV CATHOLIQUE LOUVAIN.

PI Gala J, Vannuffel P;

DR WPI; 1999-287521/24.

PS New Staphylococcus-specific oligonucleotides

XX Claim 5; Page 8; 48pp; English.

CC This invention describes novel Staphylococcus-specific oligonucleotides
 based on the consensus femA nucleotide sequence which are used to
 develop products for the identification, detection and therapy of
 infections. The oligonucleotides can be used for the genetic
 amplification, the identification and/or quantification of various femA
 sequences which are specific to known or unknown Staphylococci species.
 CC Since the femA sequence is similar to the femB sequence, the
 oligonucleotides can also be used for the molecular genotyping of femB
 genes of different Staphylococci species or other gram-positive bacteria.
 CC The femA nucleic acids can also be used in therapeutic applications.
 CC They can also be used to identify inhibitors, e.g. antibodies or
 antisense oligonucleotides, for blocking expression of the femA
 nucleotide sequences. They can also be used for producing vaccines
 against Staphylococci infections.

CC Sequence 43 BP; 19 A; 1 C; 7 G; 4 T; 12 other;

Query Match 3.2%; Score 43; DB 20; Length 43;

Best Local Similarity 100.0%; Pred. No. 4.5e-17;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 552 gnaangnaanaaanaaagtnnaanaaagtgttaaaagt 594
 |||||||||||||||||||||||||||||||||||||||

DB 1 gnaangnaanaaanaaagtnnaanaaagtgttaaaagt 43

RESULT 4

AA37762
 ID AAX37762 standard; DNA; 40 BP.

AC AAX37762;

XX 09-JUL-1999 (first entry)

DT Staphylococcus sp. detecting oligonucleotide 7.

DE FemA; primer; identification: detection; therapy: infection; femB;
 amplification; genotyping; gram-positive bacteria; vaccine; ss.

OS Synthetic.

XX Staphylococcus sp.

PN W09916780-A2.

PD 08-APR-1999.

PF 28-SEP-1998; 98MO-BE00141.

PR 26-SEP-1997; 97EP-0870146.

PA (BENA-) BELGIAN MIN NAT DEFENCE.
 (UYLO-) UNIV CATHOLIQUE LOUVAIN.

PI Gala J, Vannuffel P;

DR WPI; 1999-287521/24.

PS New Staphylococcus-specific oligonucleotides

XX Claim 5; Page 8; 48pp; English.

CC This invention describes novel Staphylococcus-specific oligonucleotides
 based on the consensus femA nucleotide sequence which are used to
 develop products for the identification, detection and therapy of
 infections. The oligonucleotides can be used for the genetic
 amplification, the identification and/or quantification of various femA
 sequences which are specific to known or unknown Staphylococci species.
 CC Since the femA sequence is similar to the femB sequence, the
 oligonucleotides can also be used for the molecular genotyping of femB
 genes of different Staphylococci species or other gram-positive bacteria.
 CC The femA nucleic acids can also be used in therapeutic applications.
 CC They can also be used to identify inhibitors, e.g. antibodies or
 antisense oligonucleotides, for blocking expression of the femA
 nucleotide sequences. They can also be used for producing vaccines
 against Staphylococci infections.

CC Sequence 40 BP; 10 A; 4 C; 6 G; 9 T; 11 other;

Query Match 3.0%; Score 40; DB 20; Length 40;

Best Local Similarity 100.0%; Pred. No. 3.5e-15;

Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 609 aagangannncnattntnngtcatatnaatgagataac 648
 |||||||||||||||||||||||||||||||||||||||

DB 1 aagangannncnattntnngtcatatnaatgagataac 40

RESULT 5

AA37756
 ID AAX37756 standard; DNA; 37 BP.

AC AAX37756;

DT 09-JUL-1999 (first entry)

DE Staphylococcus sp. detecting oligonucleotide 3.

KW FemA; primer; identification: detection; therapy: infection; femB;
 amplification; genotyping; gram-positive bacteria; vaccine; ss.

OS Synthetic

XX Staphylococcus sp.

PN WO9916780-A2.
 XX
 PD 08-APR-1999.
 XX
 PF 28-SEP-1998; 98WO-BE00141.
 XX
 PR 26-SEP-1997; 97EP-0870146.
 XX
 XX (BENA-) BELGIAN MIN NAT DEFENCE.
 PA (UYLO-) UNIV CATHOLIQUE LOUVAIN.
 XX
 PI Gala J, Vannuffel P;
 XX
 DR WPI; 1999-287521/24.
 XX
 PT New Staphylococcus-specific oligonucleotides
 XX
 PS Claim 5; Page 8; 48pp; English.
 XX
 CC This invention describes novel Staphylococcus-specific oligonucleotides
 CC based on the consensus femA nucleotide sequence which are used to
 CC develop products for the identification, detection and therapy of
 CC infections. The oligonucleotides can be used for the genetic
 CC amplification, the identification and/or quantification of various femA
 CC sequences which are specific to known or unknown Staphylococci species.
 CC Since the femA sequence is similar to the femB sequence, the
 CC oligonucleotides can also be used for the molecular genotyping of femB
 CC genes of different Staphylococci species or other gram-positive bacteria.
 CC The femA nucleic acids can also be used in therapeutic applications.
 CC They can also be used to identify inhibitors, e.g. antibodies or
 CC antisense oligonucleotides, for blocking expression of the femA
 CC nucleotide sequences. They can also be used for producing vaccines
 CC against Staphylococci infections.
 XX
 SQ Sequence 37 BP; 13 A; 1 C; 6 G; 7 T; 10 other;
 Query Match 2.8%; Score 37; DB 20; Length 37;
 Best Local Similarity 100.0%; Pred. No. 2.7e-13;
 Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 141 tagtgggnatnaanaanaataangattgattgc 177
 Db 1 tagtgggnatnaanaanaataangattgattgc 37
 RESULT 6
 AAX37772
 ID AAX37772 standard; DNA; 35 BP.
 AC AAX37772;
 XX
 DT 09-JUL-1999 (first entry)
 DE Staphylococcus sp. detecting oligonucleotide 11.
 XX
 KW FemA; primer; identification; detection; therapy; infection; femB;
 KW amplification; genotyping; gram-positive bacteria; vaccine; ss.
 XX
 OS Synthetic.
 OS Staphylococcus sp.
 PN WO9916780-A2.
 XX
 PD 08-APR-1999.
 XX
 PF 28-SEP-1998; 98WO-BE00141.
 XX
 PR 26-SEP-1997; 97EP-0870146.
 XX
 XX (BENA-) BELGIAN MIN NAT DEFENCE.
 PA (UYLO-) UNIV CATHOLIQUE LOUVAIN.
 XX
 PI Gala J, Vannuffel P;
 XX
 DR WPI; 1999-287521/24.
 XX
 PT New Staphylococcus-specific oligonucleotides
 XX
 PS Claim 5; Page 8; 48pp; English.
 XX
 CC This invention describes novel Staphylococcus-specific oligonucleotides
 CC based on the consensus femA nucleotide sequence which are used to
 CC develop products for the identification, detection and therapy of
 CC infections. The oligonucleotides can be used for the genetic
 CC amplification, the identification and/or quantification of various femA
 CC sequences which are specific to known or unknown Staphylococci species.
 CC Since the femA sequence is similar to the femB sequence, the
 CC oligonucleotides can also be used for the molecular genotyping of femB
 CC genes of different Staphylococci species or other gram-positive bacteria.
 CC The femA nucleic acids can also be used in therapeutic applications.
 CC They can also be used to identify inhibitors, e.g. antibodies or
 CC antisense oligonucleotides, for blocking expression of the femA
 CC nucleotide sequences. They can also be used for producing vaccines
 CC against Staphylococci infections.
 XX
 SQ Sequence 37 BP; 13 A; 1 C; 6 G; 7 T; 10 other;
 Query Match 2.8%; Score 37; DB 20; Length 37;
 Best Local Similarity 100.0%; Pred. No. 2.7e-13;
 Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 141 tagtgggnatnaanaanaataangattgattgc 177
 Db 1 tagtgggnatnaanaanaataangattgattgc 37
 RESULT 7
 AAX37757
 ID AAX37757 standard; DNA; 35 BP.
 AC AAX37757;
 XX
 DT 09-JUL-1999 (first entry)
 DE Staphylococcus sp. detecting oligonucleotide 4.
 XX
 KW FemA; primer; identification; detection; therapy; infection; femB;
 KW amplification; genotyping; gram-positive bacteria; vaccine; ss.
 XX
 OS Synthetic.
 OS Staphylococcus sp.
 PN WO9916780-A2.
 XX
 PD 08-APR-1999.
 XX
 PF 28-SEP-1998; 98WO-BE00141.
 XX
 PR 26-SEP-1997; 97EP-0870146.
 XX
 XX (BENA-) BELGIAN MIN NAT DEFENCE.
 PA (UYLO-) UNIV CATHOLIQUE LOUVAIN.
 XX
 PI Gala J, Vannuffel P;
 XX
 DR WPI; 1999-287521/24.
 XX
 PT New Staphylococcus-specific oligonucleotides
 XX
 PS Claim 5; Page 8; 48pp; English.
 XX
 CC This invention describes novel Staphylococcus-specific oligonucleotides
 CC based on the consensus femA nucleotide sequence which are used to
 CC develop products for the identification, detection and therapy of
 CC infections. The oligonucleotides can be used for the genetic
 CC amplification, the identification and/or quantification of various femA
 CC sequences which are specific to known or unknown Staphylococci species.
 CC Since the femA sequence is similar to the femB sequence, the
 CC oligonucleotides can also be used for the molecular genotyping of femB
 CC genes of different Staphylococci species or other gram-positive bacteria.
 CC The femA nucleic acids can also be used in therapeutic applications.
 CC They can also be used to identify inhibitors, e.g. antibodies or
 CC antisense oligonucleotides, for blocking expression of the femA
 CC nucleotide sequences. They can also be used for producing vaccines
 CC against Staphylococci infections.
 XX
 SQ Sequence 35 BP; 9 A; 3 C; 6 G; 9 T; 8 other;
 Query Match 2.6%; Score 35; DB 20; Length 35;
 Best Local Similarity 100.0%; Pred. No. 4.8e-12;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1040 agntatgcntncaatgggnnatgattgattgc 1074
 Db 1 agntatgcntncaatgggnnatgattgattgc 35
 RESULT 7
 AAX37757
 ID AAX37757 standard; DNA; 35 BP.
 AC AAX37757;
 XX
 DT 09-JUL-1999 (first entry)
 DE Staphylococcus sp. detecting oligonucleotide 4.
 XX
 KW FemA; primer; identification; detection; therapy; infection; femB;
 KW amplification; genotyping; gram-positive bacteria; vaccine; ss.
 XX
 OS Synthetic.
 OS Staphylococcus sp.
 PN WO9916780-A2.
 XX
 PD 08-APR-1999.
 XX
 PF 28-SEP-1998; 98WO-BE00141.
 XX
 PR 26-SEP-1997; 97EP-0870146.
 XX
 XX (BENA-) BELGIAN MIN NAT DEFENCE.
 PA (UYLO-) UNIV CATHOLIQUE LOUVAIN.
 XX
 PI Gala J, Vannuffel P;
 XX
 DR WPI; 1999-287521/24.
 XX
 PT New Staphylococcus-specific oligonucleotides
 XX
 PS Claim 5; Page 8; 48pp; English.
 XX
 CC This invention describes novel Staphylococcus-specific oligonucleotides
 CC based on the consensus femA nucleotide sequence which are used to
 CC develop products for the identification, detection and therapy of

CC infections. The oligonucleotides can be used for the genetic
CC amplification, the identification and/or quantification of various fema
CC sequences which are specific to known or unknown Staphylococci species.
CC Since the fema sequence is similar to the femb sequence, the
CC oligonucleotides can also be used for the molecular genotyping of femb
CC genes of different Staphylococci species or other gram-positive bacteria.
CC The fema nucleic acids can also be used in therapeutic applications.
CC They can also be used to identify inhibitors, e.g. antibodies or
CC antisense oligonucleotides, for blocking expression of the fema
CC nucleotide sequences. They can also be used for producing vaccines
CC against Staphylococci infections.

SQ Sequence 35 BP; 8 A; 3 C; 3 G; 13 T; 8 other;

Query Match 2.6%; Score 35; DB 20; Length 35;
Best Local Similarity 100.0%; Pred. No. 4.8e-12;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 197 gtcncgtnatgaanttttaantatttttc 231
|||||
1 gtcncgtnatgaanttttaantatttttc 35

Db

RESULT 8
AAx37751
ID AAX37751 standard; DNA; 35 BP.
AC AAX37751;
XX
DT 09-JUL-1999 (first entry)
XX
DE Staphylococcus sp. detecting oligonucleotide 1.
XX
KW FemA; primer; identification; detection; therapy; infection; femB;
KW amplification; genotyping; gram-positive bacteria; vaccine; ss.
XX
OS Synthetic.
OS Staphylococcus sp.
XX
PN W09916780-A2.
XX
PD 08-APR-1999.
XX
PF 28-SEP-1998; 98WO-BE00141.
XX
PR 26-SEP-1997; 97EP-0870146.
XX
XX (BENA-) BELGIAN MIN NAT DEFENCE.
PA (UYLO-) UNIV CATHOLIQUE LOUVAIN.
XX
PI Gala J, Vannuffel P;
XX
DR WPI; 1999-287521/24.
XX
PT New Staphylococcus-specific oligonucleotides
PS Claim 5; Page 8; 48pp; English.
XX
CC This invention describes novel Staphylococcus-specific oligonucleotides
CC based on the consensus fema nucleotide sequence which are used to
CC develop products for the identification, detection and therapy of
CC infections. The oligonucleotides can be used for the genetic
CC amplification, the identification and/or quantification of various fema
CC sequences which are specific to known or unknown Staphylococci species.
CC Since the fema sequence is similar to the femb sequence, the
CC oligonucleotides can also be used for the molecular genotyping of femb
CC genes of different Staphylococci species or other gram-positive bacteria.
CC The fema nucleic acids can also be used in therapeutic applications.
CC They can also be used to identify inhibitors, e.g. antibodies or
CC antisense oligonucleotides, for blocking expression of the fema
CC nucleotide sequences. They can also be used for producing vaccines
CC against Staphylococci infections.

XX SQ Sequence 35 BP; 12 A; 3 C; 3 G; 9 T; 8 other;

Query Match 2.6%; Score 35; DB 20; Length 35;
Best Local Similarity 100.0%; Pred. No. 4.8e-12;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 14 anaatgaantttacnaattttacngcnaagant 48
|||||
1 anaatgaantttacnaattttacngcnaagant 35

Db

RESULT 9
AAx37764
ID AAX37764 standard; DNA; 32 BP.
AC AAX37764;
XX
DT 09-JUL-1999 (first entry)
XX
DE Staphylococcus sp. detecting oligonucleotide 9.
XX
KW FemA; primer; identification; detection; therapy; infection; femB;
KW amplification; genotyping; gram-positive bacteria; vaccine; ss.
XX
OS Synthetic.
OS Staphylococcus sp.
XX
PN W09916780-A2.
XX
PD 08-APR-1999.
XX
PF 28-SEP-1998; 98WO-BE00141.
XX
PR 26-SEP-1997; 97EP-0870146.
XX
XX (BENA-) BELGIAN MIN NAT DEFENCE.
PA (UYLO-) UNIV CATHOLIQUE LOUVAIN.
XX
PI Gala J, Vannuffel P;
XX
DR WPI; 1999-287521/24.
XX
PT New Staphylococcus-specific oligonucleotides
PS Claim 5; Page 9; 48pp; English.
XX
CC This invention describes novel Staphylococcus-specific oligonucleotides
CC based on the consensus fema nucleotide sequence which are used to
CC develop products for the identification, detection and therapy of
CC infections. The oligonucleotides can be used for the genetic
CC amplification, the identification and/or quantification of various fema
CC sequences which are specific to known or unknown Staphylococci species.
CC Since the fema sequence is similar to the femb sequence, the
CC oligonucleotides can also be used for the molecular genotyping of femb
CC genes of different Staphylococci species or other gram-positive bacteria.
CC The fema nucleic acids can also be used in therapeutic applications.
CC They can also be used to identify inhibitors, e.g. antibodies or
CC antisense oligonucleotides, for blocking expression of the fema
CC nucleotide sequences. They can also be used for producing vaccines
CC against Staphylococci infections.

SQ Sequence 32 BP; 16 A; 2 C; 4 G; 1 T; 9 other;

Query Match 2.4%; Score 32; DB 20; Length 32;
Best Local Similarity 100.0%; Pred. No. 3.7e-10;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 818 aanganatnganaaangcncnganaaaaaa 849
|||||
1 aanganatnganaaangcncnganaaaaaa 32

us-09-509-234c-1.oligol5.rng

Wed Jun 26 10:05:17 2002

```

RESULT 10
AAX37771
ID AAX37771 standard; DNA; 32 BP.
XX
AC AAX37771;
XX
DT 09-JUL-1999 (first entry)
XX
DE Staphylococcus sp. detecting oligonucleotide 10.
XX
XX FemA; primer; identification; detection; therapy; infection; femB;
KW amplification; genotyping; gram-positive bacteria; vaccine; ss.
XX
OS Synthetic.
XX
OS Staphylococcus sp.
XX
PN WO9916780-A2.
XX
PD 08-APR-1999.
XX
XX 28-SEP-1998; 98WO-BE00141.
XX
XX 26-SEP-1997; 97EP-0870146.
XX
XX (BENA-) BELGIAN MIN NAT DEFENCE.
PA (UYLO-) UNIV CATHOLIQUE LOUVAIN.
XX
XX Gala J, Vannuffel P;
PI
XX WPI; 1999-287521/24.
XX
XX New Staphylococcus-specific oligonucleotides
XX
XX Claim 5; Page 8; 48pp; English.
XX
XX This invention describes novel Staphylococcus-specific oligonucleotides
CC based on the consensus femA nucleotide sequence which are used to
CC develop products for the identification, detection and therapy of
CC infections. The oligonucleotides can be used for the genetic
CC amplification, the identification and/or quantification of various femA
CC sequences which are specific to known or unknown Staphylococci species.
CC Since the femA sequence is similar to the femB sequence, the
CC oligonucleotides can also be used for the molecular genotyping of femB
CC genes of different Staphylococci species or other gram-positive bacteria.
CC The femA nucleic acids can also be used in therapeutic applications.
CC They can also be used to identify inhibitors, e.g. antibodies or
CC antisense oligonucleotides, for blocking expression of the femA
CC nucleotide sequences. They can also be used for producing vaccines
CC against Staphylococci infections.
XX
SQ Sequence 32 BP; 6 A; 3 C; 8 G; 8 T; 7 other;

Query Match 2.4%; Score 32; DB 20; Length 32;
Best Local Similarity 100.0%; Pred. No. 3.7e-10;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 977 aatccntntgaagtnttantangcnggtgg 1008
   |||||
Db 1 aatccntntgaagtnttantangcnggtgg 32

RESULT 11
AAX37754
ID AAX37754 standard; DNA; 25 BP.
XX
AC AAX37754;
XX
DT 09-JUL-1999 (first entry)
XX
DE Staphylococcus sp. detecting oligonucleotide 2.
XX
XX FemA; primer; identification; detection; therapy; infection; femB;
KW amplification; genotyping; gram-positive bacteria; vaccine; ss.
XX
OS Synthetic.
XX
OS Staphylococcus sp.
XX
PN WO9916780-A2.
XX
PD 08-APR-1999.
XX
XX 28-SEP-1998; 98WO-BE00141.
XX
XX 26-SEP-1997; 97EP-0870146.
XX
XX (BENA-) BELGIAN MIN NAT DEFENCE.
PA (UYLO-) UNIV CATHOLIQUE LOUVAIN.
XX
XX Gala J, Vannuffel P;
PI
XX WPI; 1999-287521/24.
XX
XX New Staphylococcus-specific oligonucleotides
XX
XX Claim 5; Page 9; 48pp; English.
XX
XX This invention describes novel Staphylococcus-specific oligonucleotides
CC based on the consensus femA nucleotide sequence which are used to
CC develop products for the identification, detection and therapy of
CC infections. The oligonucleotides can be used for the genetic
CC amplification, the identification and/or quantification of various femA
CC sequences which are specific to known or unknown Staphylococci species.
CC Since the femA sequence is similar to the femB sequence, the
CC oligonucleotides can also be used for the molecular genotyping of femB
CC genes of different Staphylococci species or other gram-positive bacteria.
CC The femA nucleic acids can also be used in therapeutic applications.
CC They can also be used to identify inhibitors, e.g. antibodies or
CC antisense oligonucleotides, for blocking expression of the femA
CC nucleotide sequences. They can also be used for producing vaccines
CC against Staphylococci infections.
XX
SQ Sequence 32 BP; 6 A; 3 C; 8 G; 8 T; 7 other;

Query Match 1.9%; Score 25; DB 20; Length 25;
Best Local Similarity 100.0%; Pred. No. 9.2e-06;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 atgcnncnagncatttnacncana 92
   |||||
Db 1 atgcnncnagncatttnacncana 25

RESULT 12
AAX37753
ID AAX37753 standard; cDNA; 413 BP.
XX
AC AAX37753;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human polynucleotide SEQ ID NO 5653.
XX
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation; ss.
XX
OS Homo sapiens.
XX
PN WO200164835-A2.
XX
PD 07-SEP-2001.

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PR 23-MAY-1991; 91US-0704814.
PR 20-SEP-1991; 91US-0763039.
PR 22-MAY-1992; 92US-0887502.
PR 23-NOV-1993; 93US-0157811.
XX
XX (MART/) MARTIN W J.
XX Martin WJ;
XX
XX WPI; 1998-311405/27.
XX
XX Stealth virus contained in MRC-5 cell line, ATCC number VR2343 - is
XX useful as a vaccine against chronic fatigue syndrome
XX
XX Disclosure; Fig 1D; 99pp; English.
XX
XX AAV11954-V12024 are plasmids which contain fragments of a stealth virus
XX isolated from a patient, D.W. Such stealth virus fragments can be used
XX as vaccine against chronic fatigue syndrome (CFS). This illness causes
XX unexplained fatigue lasting more than 6 months and greater than 50%
XX reduction in an infected persons normal level of activity. The virus
XX causes a cytopathic effect (CPE) to fibroblast cells observed in
XX culture, characterised by the appearance of rounded, slightly enlarged,
XX refractile cells in the culture.
XX
XX Sequence 737 BP; 118 A; 158 C; 120 G; 129 T; 212 other;
SQ

Query Match 1.7%; Score 23; DB 19; Length 737;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1283 nnnnnnnnnnnnnnnnnnnnnnn 1305
Db 678 NNNNNNNNNNNNNNNNNNNNNNN 656

RESULT 15
AAV10153/c
ID AAV10153 standard; DNA; 737 BP.
XX
XX AAV10153;
XX
XX 29-MAY-1998 (first entry)
XX
XX Stealth virus nucleic acid in plasmid #13.
XX
XX Stealth virus; chronic fatigue syndrome; CFS; disease; detection;
XX medical diagnostic; veterinary diagnostic; agricultural diagnostic;
XX quality control; ss.
XX
XX Stealth virus.
XX
XX US5703221-A.
XX
XX 30-DEC-1997.
XX
XX 05-JUN-1995; 95US-0463115.
XX
XX 05-JUN-1995; 95US-0463115.
XX 23-MAY-1991; 91US-0704814.
XX 20-SEP-1991; 91US-0763039.
XX 22-MAY-1992; 92US-0887502.
XX 23-NOV-1993; 93US-0157811.
XX
XX (MART/) MARTIN W J.
XX Martin WJ;
XX
XX WPI; 1998-076485/07.
XX
XX Stealth virus nucleic acid molecule - useful to detecting stealth
XX virus, e g in chronic fatigue syndrome diagnosis
PT
```

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XX
XX Example 5; Fig 1; 82pp; English.
XX
XX AAV10141-V10210 represent nucleic acid sequences obtained from a
XX patient with a stealth virus infection, namely chronic fatigue
XX syndrome (CFS). Such nucleic acid sequences can be used to detect
XX the stealth virus in medical, veterinary and agricultural diagnostics
XX and in industrial and pharmaceutical biological quality control, e.g.
XX to diagnose a disease associated with the stealth virus.
XX
XX Sequence 737 BP; 118 A; 158 C; 120 G; 129 T; 212 other;
SQ

Query Match 1.7%; Score 23; DB 19; Length 737;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1283 nnnnnnnnnnnnnnnnnnnnnnn 1305
Db 678 NNNNNNNNNNNNNNNNNNNNNNN 656

Search completed: June 22, 2002, 07:54:45
Job time: 7424 sec
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Query Match 1.7%; Score 23; DB 1; Length 737;
Best Local Similarity 100.0%; Pred. No. 2.6e-05;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1283 nnnnnnnnnnnnnnnnnnnnn 1305
|||||
DB 678 nnnnnnnnnnnnnnnnnnnnn 656

RESULT 2
US-08-465-388-19/c
; Sequence 19, Application US/08465388
; Patent No. 5753488
; GENERAL INFORMATION:
; APPLICANT: WILLIAM JOHN MARTIN
; TITLE OF INVENTION: ISOLATED STEALTH VIRUSES
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; COUNTRY: California
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,388
; FILING DATE: June 5, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: Including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 08/157,811
; FILING DATE: No. 5753488ember 23, 1993
; APPLICATION NUMBER: 07/887,502
; FILING DATE: May 22, 1992
; APPLICATION NUMBER: 07/704,814
; FILING DATE: May 23, 1991
; APPLICATION NUMBER: 07/763,039
; FILING DATE: September 20, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Waiburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 213/300
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELETYPE: 67-3510
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 737 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION:
US-08-465-388-19

Query Match 1.7%; Score 23; DB 1; Length 737;
Best Local Similarity 100.0%; Pred. No. 2.6e-05;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1283 nnnnnnnnnnnnnnnnnnnnn 1305
|||||

DB 678 nnnnnnnnnnnnnnnnnnnnn 656

RESULT 3
US-08-358-810A-16/c
; Sequence 16, Application US/08358810A
; Patent No. 5604097
; GENERAL INFORMATION:
; APPLICANT: Sydney Brenner
; TITLE OF INVENTION: Molecular Tagging System
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen C. Macevicz, Lynx Therapeutics, Inc.
; STREET: 3832 Bay Center Place
; CITY: Hayward
; STATE: California
; COUNTRY: USA
; ZIP: 94545
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: Macintosh
; OPERATING SYSTEM: Mac OS
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,810A
; FILING DATE: 19-DEC-94
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/322,348
; FILING DATE: 13-OCT-94
; ATTORNEY/AGENT INFORMATION:
; NAME: Stephen C. Macevicz
; REGISTRATION NUMBER: 30,285
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 670-9365
; TELEFAX: (510) 670-9302
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-358-810A-16

Query Match 1.2%; Score 16; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 0.86;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1291 nnnnnnnnnnnnnnnnnnnnn 1306
|||||
DB 28 nnnnnnnnnnnnnnnnnnnnn 13

RESULT 4
US-08-484-712A-16/c
; Sequence 16, Application US/08484712A
; Patent No. 5654413
; GENERAL INFORMATION:
; APPLICANT: Sydney Brenner
; TITLE OF INVENTION: Compositions for Sorting Polynucleotides
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen C. Macevicz, Lynx Therapeutics, Inc.
; STREET: 3832 Bay Center Place
; CITY: Hayward
; STATE: California
; COUNTRY: USA
; ZIP: 94545
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: Macintosh

OPERATING SYSTEM: Mac OS
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,712A
FILING DATE: 07-JUN-95
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/322,348
FILING DATE: 13-OCT-94
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/358,810
FILING DATE: 19-DEC-94
ATTORNEY/AGENT INFORMATION:
NAME: Stephen C. Macevicz
REGISTRATION NUMBER: 30,285
REFERENCE/DOCKET NUMBER: cbd2c2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 670-9365
TELEFAX: (510) 670-9302
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 nucleotides
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-484-712A-16

Query Match 1.2%; Score 16; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 0.86;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1291 nnnnnnnnnnnnn 1306
Db 28 NNNNNNNNNNNNN 13

RESULT 5
US-08-359-295C-22/c
; Sequence 22, Application US/08359295C
; Patent No. 5695934
; GENERAL INFORMATION:
; APPLICANT: Sydney Brenner
; TITLE OF INVENTION: Massively Parallel Sequencing of Sorted Polynucleotides
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen C. Macevicz, Lynx Therapeutics, Inc.
; STREET: 3832 Bay Center Place
; CITY: Hayward
; STATE: California
; COUNTRY: USA
; ZIP: 94545
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 3.1
; SOFTWARE: Microsoft Word 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/359,295C
; FILING DATE: 19-DEC-94
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/322,348
; FILING DATE: 13-OCT-94
; ATTORNEY/AGENT INFORMATION:
; NAME: Stephen C. Macevicz
; REGISTRATION NUMBER: 30,285
; REFERENCE/DOCKET NUMBER: mps1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 670-9365
; TELEFAX: (510) 670-9302
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-484-712A-16

LENGTH: 37 nucleotides
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-359-295C-22

Query Match 1.2%; Score 16; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 0.86;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1291 nnnnnnnnnnnnn 1306
Db 28 NNNNNNNNNNNNN 13

RESULT 6
US-08-485-105A-22/c
; Sequence 22, Application US/08485105A
; Patent No. 5863722
; GENERAL INFORMATION:
; APPLICANT: Sydney Brenner
; TITLE OF INVENTION: Massively Parallel Sequencing of Sorted Polynucleotides
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen C. Macevicz, Lynx Therapeutics, Inc.
; STREET: 3832 Bay Center Place
; CITY: Hayward
; STATE: California
; COUNTRY: USA
; ZIP: 94545
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 3.1
; SOFTWARE: Microsoft Word 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,105A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/359,295
; FILING DATE: 19-DEC-94
; APPLICATION NUMBER: 08/322,348
; FILING DATE: 13-OCT-94
; ATTORNEY/AGENT INFORMATION:
; NAME: Stephen C. Macevicz
; REGISTRATION NUMBER: 30,285
; REFERENCE/DOCKET NUMBER: mps1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 670-9365
; TELEFAX: (510) 670-9302
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-485-105A-22

Query Match 1.2%; Score 16; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 0.86;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1291 nnnnnnnnnnnnn 1306
Db 28 NNNNNNNNNNNNN 13

RESULT 7
US-09-183-650-22/c
; Sequence 22, Application US/09183650B

```

: Patent No.6140489
:
: GENERAL INFORMATION:
: APPLICANT: Brenner, Sydney
: TITLE OF INVENTION: Improved compositions for sorting polynucleotides
: FILE REFERENCE: 803-03
: CURRENT APPLICATION NUMBER: US/09/183,650B
: CURRENT FILING DATE: 1998-10-30
: EARLIER APPLICATION NUMBER: US 08/485,105
: EARLIER FILING DATE: 1995-06-07
: EARLIER APPLICATION NUMBER: US 08/359,295
: EARLIER FILING DATE: 1994-12-19
: EARLIER APPLICATION NUMBER: US 08/322,348
: EARLIER FILING DATE: 1994-10-13
: NUMBER OF SEQ ID NOS: 23
: SOFTWARE: Microsoft Word97
: SEQ ID NO 22
:
: LENGTH: 37
:
: TYPE: DNA
:
: ORGANISM: Artificial Sequence
: FEATURE: No. 6140489special biological significance.
: NAME/KEY: Primer.
: LOCATION: five 5' nucleotides; 13 central nucleotides; 13 3' nucleotides
: OTHER INFORMATION: Tag-containing primer.
:
: US-09-183-650-22

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Query Match 1.2%; Score 16; DB 3; Length 37;
Best Local Similarity 100.0%; Pred. No. 0.86;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0

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QY 1291 nnnnnnnnnnnnnnnnn 1306
    | | | | | | | | | | | | | |
Db 28 NNNNNNNNNNNNNNNNN 13
```

RESULT 8
US-09-115-446-4
; Sequence 4, Application US/09115446

```

1 GENERAL INFORMATION:
2 APPLICANT: Chandry, George K.
3 APPLICANT: Gargus, Jay J.
4 APPLICANT: Gutman, George
5 APPLICANT: Paolino, Emmanuelle
6 APPLICANT: Kalman, Katarin
7 TITLE OF INVENTION: HRCAL/KCNC3 SMALL CONDUCTANCE CALCIUM
8 TITLE OF INVENTION: ACTIVATED POTASSIUM CHANNEL: A DIAGNOSTIC
9 FILE REFERENCE: 07306/014001
10 CURRENT APPLICATION NUMBER: US/09/115,446
11 EARLIER FILING DATE: 1998-07-14
12 EARLIER APPLICATION NUMBER: 60/052,556
13 EARLIER FILING DATE: 1997-07-15
14 EARLIER APPLICATION NUMBER: 60/070,741
15 EARLIER FILING DATE: 1998-01-08
16 NUMBER OF SEQ. ID NOS: 15
17 SOFTWARE: FastSeq for Windows Version 4.0
18 SEQ. ID NOS:

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; SEQ ID NO 4
; LENGTH: 72
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-115-446-4

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Query Match      1.28; Score 16; DB 4; Length 72;
Best Local Similarity 100.08; Pred. No. 0.76;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1291 nnnnnnnnnnnnnnnnn 1306
Db 24 nnnnnnnnnnnnnnnnn 39
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RESULT      9
US-09-417-455-1
; Sequence 1, Application US/09417455
; Patent No. 6294655
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Page and

```

```

1 FILE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USUS THEREOF
2 FILE REFERENCE: 28110/36328
3 CURRENT APPLICATION NUMBER: US/09/417,455
4 CURRENT FILING DATE: 1999-10-13
5 PRIOR APPLICATION NUMBER: US 09/348,942
6 PRIOR FILING DATE: 1999-07-07
7 PRIOR APPLICATION NUMBER: PCT/US99/04291
8 PRIOR FILING DATE: 1999-04-05
9 PRIOR APPLICATION NUMBER: US 09/287,210
10 PRIOR FILING DATE: 1999-04-05
11 PRIOR APPLICATION NUMBER: US 09/251,370
12 PRIOR FILING DATE: 1999-02-17
13 PRIOR APPLICATION NUMBER: US 09/229,591
14 PRIOR FILING DATE: 1999-01-13
15 PRIOR APPLICATION NUMBER: US 09/127,698
16 PRIOR FILING DATE: 1998-07-31
17 PRIOR APPLICATION NUMBER: US 09/099,818
18 PRIOR FILING DATE: 1998-06-19
19 PRIOR APPLICATION NUMBER: US 09/082,364
20 PRIOR FILING DATE: 1998-05-20
21 PRIOR APPLICATION NUMBER: US 09/079,909
22 PRIOR FILING DATE: 1998-05-15
23 PRIOR APPLICATION NUMBER: US 09/055,010
24 PRIOR FILING DATE: 1998-04-03
25 NUMBER OF SEQ ID NOS: 30
26 SOFTWARE: FastSeq for Windows Version 3.0
27 SEQ ID NO 1
28 LENGTH: 357
29 TYPE: DNA
30 ORGANISM: Homo sapiens
31 FEATURE:
32 NAME/KEY: misc_feature
33 LOCATION: (1)...(357)
34 OTHER INFORMATION: n = A,T,C or G
35 JS-09-417-455-1

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Query Match:          1.2%;  Score 16;  DB 4;  Length 357;
Best Local Similarity 100.0%;  Pired. NO. 0.56;
Matches 16;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
QY 1291 nnnnnnnnnnnnnnnnn 1306
      | | | | | | | | | | | | | |
Db 336 nnnnnnnnnnnnnnnnn 351

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RESULT 10
US-09-348-942-1
; Sequence 1, Application US/09348942
; Patent No. 6337072
; GENERAL INFORMATION:
; APPLICANT: John Ford
; TITLE OF INVENTION: A NOVEL, INTERI

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; EARLIER APPLICATION NUMBER: US 09/099,818
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: US 09/082,364
; EARLIER FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: US 09/079,909
; EARLIER FILING DATE: 1998-05-15
; EARLIER APPLICATION NUMBER: US 09/055,010
; EARLIER FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 357
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(357)
; OTHER INFORMATION: n = A,T,C or G
US-09-348-942-1

Query Match 1.2%; Score 16; DB 4; Length 357;
Best Local Similarity 100.0%; Pred. No. 0.56;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1291 nnnnnnnnnnnnnnn 1306
|||||
Db 336 nnnnnnnnnnnnnnn 351

RESULT 11
US-09-109-205-8
; Sequence 8, Application US/09109205
; Patent No. 6057140
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Guegler, Karl J.
; APPLICANT: Gorgone, Gina
; APPLICANT: Corley, Neil C.
; APPLICANT: Baughn, Mariah R.
; APPLICANT: Yue, Henry
; TITLE OF INVENTION: HUMAN SCAD FAMILY MOLECULES
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/109,205
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cerrone, Michael C
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0542 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-855-0572
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 555 base pairs

; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: LUNGUT10
; CLONE: 2722958F6
US-09-109-205-8

Query Match 1.2%; Score 16; DB 3; Length 555;
Best Local Similarity 100.0%; Pred. No. 0.52;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1291 nnnnnnnnnnnnnnn 1306
|||||
Db 492 NNNNNNNNNNNNNNN 507

RESULT 12
US-08-647-368A-3/C
; Sequence 3, Application US/08647368A
; Patent No. 5928906
; GENERAL INFORMATION:
; APPLICANT: Koster, Hubert
; APPLICANT: Van de Boom, Dirk
; APPLICANT: Ruppert, Andreas
; TITLE OF INVENTION: PROCESS FOR DIRECT SEQUENCING DURING
; TITLE OF INVENTION: TEMPLATE AMPLIFICATION
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/647,368A
; FILING DATE: 09-MAY-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: SOA-020.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 558 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-647-368A-3

Query Match 1.2%; Score 16; DB 2; Length 558;
Best Local Similarity 100.0%; Pred. No. 0.52;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1291 nnnnnnnnnnnnnnn 1306
|||||
Db 27 NNNNNNNNNNNNNNN 12

RESULT 13
US-08-781-550-35/c


```

Sequence 35, Application US/08781550
Patent No. 5861242
GENERAL INFORMATION:
APPLICANT: Chee, Mark
APPLICANT: Gingersas, Thomas R.
APPLICANT: Fodor, Stephen P.A.
APPLICANT: Hubbell, Earl A.
APPLICANT: Morris, Macdonald S.
TITLE OF INVENTION: HIV Diagnosis by Arrays of Nucleic Acid
TITLE OF INVENTION: Probes on Biological Chips
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourile and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,550
FILING DATE: 09-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/284,064
FILING DATE: 02-AUG-1994
APPLICATION NUMBER: US 08/143,312
FILING DATE: 26-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/082,937
FILING DATE: 25-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Stevens, Lauren D.
REGISTRATION NUMBER: 36,691
REFERENCE/DOCKET NUMBER: 1046.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 831 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (oligonucleotide)
US-08-781-550-35

Query Match          1.2%; Score 16; DB 2; Length 831;
Best Local Similarity 100.0%; Pred. No. 0.48;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY   1291 nnnnnnnnnnnnnn 1306
      |||||
Db    60 nnnnnnnnnnnnnnnn 45

RESULT 14
Sequence 36, Application US/08781550
Patent No. 5861242
GENERAL INFORMATION:
APPLICANT: Chee, Mark
APPLICANT: Gingersas, Thomas R.
APPLICANT: Fodor, Stephen P.A.
APPLICANT: Hubbell, Earl A.
APPLICANT: Morris, Macdonald S.
TITLE OF INVENTION: HIV Diagnosis by Arrays of Nucleic Acid
TITLE OF INVENTION: Probes on Biological Chips

```

```

NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourile and Crew
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,550
FILING DATE: 09-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/284,064
FILING DATE: 02-AUG-1994
APPLICATION NUMBER: US 08/143,312
FILING DATE: 26-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/082,937
FILING DATE: 25-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Stevens, Lauren L.
REGISTRATION NUMBER: 36,691
REFERENCE/DOCKET NUMBER: 1046.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 831 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (oligonucleotide)
US-08-781-550-36

Query Match      1.2%; Score 16; DB 2; Length 831;
Best Local Similarity 100.0%; Pred. No. 0.48;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 1291 nnnnnnnnnnnnnna 1306
   |||||
Db 51 NNNNNNNNNNNNNN 36

RESULT 15
US-08-642-807A-32
Sequence 32, Application US/08642807A
Patent No. 6087097
GENERAL INFORMATION:
APPLICANT: Persing, D. H.
TITLE OF INVENTION: PCR DETECTION OF BORRELIA
TITLE OF INVENTION: BURGDOFFERI
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schweegman, Lundberg, Woessner & Kluth, P.A.
STREET: P.O. Box 2938
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 22, 2002, 05:48:26 ; Search time 1732.11 Seconds
(without alignments)
10348.047 Million cell updates/sec

Title: US-09-509-234C-1

Perfect score: 1328

Sequence: 1 nnnnnnnnnnnanaatga.....gaaattacagaggttaannn 1328

Scoring table:
OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 13736207 seqs, 6748477542 residues

Word size : 15

Total number of hits satisfying chosen parameters: 8275

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

EST:*

1: em_estba: *
2: em_esthum: *
3: em_estin: *
4: em_estmu: *
5: em_estov: *
6: em_estpl: *
7: em_estro: *
8: em_hic: *
9: gb_esti: *
10: gb_est2: *
11: gb_hic: *
12: gb_gss: *
13: em_gss_hum: *
14: em_gss_inv: *
15: em_gss_pln: *
16: em_gss_vrt: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	26	2.0	698	12	AQ688088 nbxb0076N
C 2	26	2.0	778	12	A2186959 SP_1008_A
C 3	26	2.0	790	12	AQ325762 nbxb0021K
C 4	25	1.9	463	12	BH213183 SALK_0088
C 5	25	1.9	489	12	A2165463 SP_0082_A
C 6	25	1.9	558	12	AQ328561 nbxb0043K
C 7	25	1.9	645	10	W27482
C 8	25	1.9	1019	3	Bi644649 Op2409 M1
C 9	24	1.8	87	12	BH618435
C 10	24	1.8	159	12	CNS01300
C 11	24	1.8	326	12	CNS009YW
C 12	24	1.8	337	10	BM270207
C 13	24	1.8	359	12	CNS0027H
C 14	24	1.8	372	9	AQ977493
C 15	24	1.8	372	12	AQ090902
C 16	24	1.8	425	12	CNS07GRP
C 17	24	1.8	430	12	BH618532

18	24	1.8	433	12	AG171193
C 19	24	1.8	479	12	AZ148060
C 20	24	1.8	509	9	BE134884
C 21	24	1.8	543	12	AQ772807
C 22	24	1.8	553	12	BH023388
C 23	24	1.8	579	10	W27379
C 24	24	1.8	595	12	AQ256216
C 25	24	1.8	597	12	AQ363651
C 26	24	1.8	605	9	AI529149
C 27	24	1.8	640	10	BE427117
C 28	24	1.8	673	12	AQ578218
C 29	24	1.8	674	10	W27605
C 30	24	1.8	679	10	W27163
C 31	24	1.8	689	10	W22075
C 32	24	1.8	704	12	B21357
C 33	24	1.8	705	9	AI907070
C 34	24	1.8	708	12	AZ200367
C 35	24	1.8	712	12	AQ361799
C 36	24	1.8	713	12	AQ331063
C 37	24	1.8	717	12	AG011405
C 38	24	1.8	720	12	AZ197399
C 39	24	1.8	722	12	AZ199635
C 40	24	1.8	731	12	AZ200525
C 41	24	1.8	732	9	AI907056
C 42	24	1.8	736	12	AQ991674
C 43	24	1.8	745	12	AQ738773
C 44	24	1.8	750	12	AQ365752
C 45	24	1.8	759	10	D43354
C 46	24	1.8	759	12	B12963
C 47	24	1.8	764	10	W25977
C 48	24	1.8	767	12	AQ576024
C 49	24	1.8	773	12	AQ861387
C 50	24	1.8	778	10	BF866205
C 51	24	1.8	779	10	W27471
C 52	24	1.8	791	12	AZ046289
C 53	24	1.8	794	9	BE033700
C 54	24	1.8	796	10	W22165
C 55	24	1.8	797	10	W27460
C 56	24	1.8	803	10	W27419
C 57	24	1.8	808	12	B18870
C 58	24	1.8	811	12	AQ744675
C 59	24	1.8	813	12	AQ744721
C 60	24	1.8	815	12	AQ858408
C 61	24	1.8	822	12	AQ740151
C 62	24	1.8	826	10	W28431
C 63	24	1.8	826	10	W28611
C 64	24	1.8	835	12	AG095014
C 65	24	1.8	836	10	W28599
C 66	24	1.8	882	12	AZ184391
C 67	24	1.8	925	10	W26625
C 68	24	1.8	936	10	W28482
C 69	24	1.8	940	12	B09308
C 70	24	1.8	944	12	AQ749273
C 71	24	1.8	992	12	AQ745316
C 72	24	1.8	995	12	BF272432
C 73	24	1.8	1015	9	AI438239
C 74	24	1.8	1016	10	BM473972
C 75	24	1.8	1018	10	BF178319
C 76	24	1.8	1060	12	CNS0076A
C 77	24	1.8	1082	9	AI438238
C 78	24	1.8	1095	12	AQ741834
C 79	24	1.8	1101	12	CNS002R8
C 80	24	1.8	1114	9	AI539890
C 81	24	1.8	1189	12	AG040366
C 82	24	1.8	1204	10	BM452144
C 83	24	1.8	1244	10	BE422228
C 84	24	1.8	1320	12	AG038111
C 85	24	1.8	2663	9	AW727897
C 86	23	1.7	453	12	AG857736
C 87	23	1.7	503	10	BF890898
C 88	23	1.7	506	12	AZ143700
C 89	23	1.7	509	12	AQ915477
C 90	23	1.7	560	9	AV858241

C 91	23	1.7	687	12	AG069287	Pan	trog1	C 164	20	1.5	131	12	CNS00865	AL051776	Drosoph11
C 92	23	1.7	688	12	AQ740348	HS_5501_A		C 165	20	1.5	166	12	BH254397	BH254397	SALK_0164
C 93	23	1.7	701	12	B11978	T2L16-SP6_T		C 166	20	1.5	173	12	BH214251	BH214251	SALK_0104
C 94	23	1.7	719	12	AO853742	AO853742 nbxb0032G		C 167	20	1.5	325	9	AI973642	AI973642	sd07f12.y
C 95	23	1.7	719	12	B21675	B21675 F17P15-SP6		C 168	20	1.5	327	9	AW147400	AW147400	da02609.y
C 96	23	1.7	738	12	AQ781271	HS_3138_A		C 169	20	1.5	334	12	AO097945	AO097945	HS_3041_A
C 97	23	1.7	747	10	W25796	W25796 13110 Human		C 170	20	1.5	439	12	B1084007	B1084007	B1084007
C 98	23	1.7	773	10	BF317597	BF317597 24G-4-23		C 171	20	1.5	439	12	BH253591	BH253591	SALK_0151
C 99	23	1.7	795	10	W28793	W28793 5214 Human		C 172	20	1.5	452	12	BH633265	BH633265	
C 100	23	1.7	803	12	AG088882	AG088882 Pan	trog1	C 173	20	1.5	471	12	AO887414	AO887414	HS_5555_A
C 101	23	1.7	825	12	AG088882	AG088882 Pan	trog1	C 174	20	1.5	563	12	AW959203	AW959203	EST371273
C 102	23	1.7	833	12	AO745562	AO745562 HS_2272.A		C 175	20	1.5	563	12	AQ272648	AQ272648	nbxb0028B
C 103	23	1.7	872	9	AI353051	AI353051 SMOVAFCAP		C 176	20	1.5	569	12	AZ142637	AZ142637	SP_0041_B
C 104	23	1.7	878	12	B20048	B20048 T16G2-T7_TA		C 177	20	1.5	580	12	CNS013HO	AL102870	Drosoph11
C 105	23	1.7	907	12	B09953	B09953 F1H12-SP6_T		C 178	20	1.5	580	12	AO336620	AO336620	HS_5018_B
C 106	23	1.7	1018	9	AI438763	AI438763 SMOV3MCM		C 179	20	1.5	612	12	BH023385	BH023385	GH_MBD000
C 107	23	1.7	1143	12	B12536	B12536 F1K23-T7_IG		C 180	20	1.5	612	12	W26291	W26291	25G2 Human
C 108	23	1.7	1202	9	AI539904	AI539904 SMOVAFCAP		C 181	20	1.5	628	12	AQ288634	AQ288634	nbxb0017F
C 109	23	1.7	1702	9	BE055453	BE055453 GA_EA003		C 182	20	1.5	637	12	AG009827	AG009827	Hom sapi
C 110	22	1.7	188	12	CNS01003	AL098349 Drosoph11		C 183	20	1.5	641	9	AI547050	AI547050	PN2.1_1_B
C 111	22	1.7	304	12	BH612150	BH612150 SALK_0322		C 184	20	1.5	670	10	W22080	W22080	61C9 Human
C 112	22	1.7	422	12	BH631185	BH631185 SALK_0403		C 185	20	1.5	684	12	B10022	B10022	SP_0141_A
C 113	22	1.7	436	12	BH634298	BH634298 SALK_0451		C 186	20	1.5	684	12	AZ176320	AZ176320	SP_0141_A
C 114	22	1.7	436	12	AW133468	AW133468 sel19d11.y		C 187	20	1.5	703	12	AQ330422	AQ330422	nbxb0047M
C 115	22	1.7	449	12	BH611543	BH611543 SALK_0311		C 188	20	1.5	712	12	AG159627	AG159627	Hom sapi
C 116	22	1.7	477	12	BH611243	BH611243 SALK_0305		C 189	20	1.5	723	12	AG012448	AG012448	Drosoph11
C 117	22	1.7	481	12	BH171615	BH171615 SALK_0045		C 190	20	1.5	738	12	CNS00EOH	B12102	F27F4-T7_IG
C 118	22	1.7	484	10	H15527	H15527 ym27a06.s1		C 191	20	1.5	883	12	AZ200357	AZ200357	SP_1002_B
C 119	22	1.7	503	12	AQ446291	AQ446291 nbxb00691		C 192	20	1.5	900	12	CNS0163B	AL106817	Drosoph11
C 120	22	1.7	592	12	AQ431768	AQ431768 HS_5061_A		C 193	20	1.5	921	9	BE036013	BE036013	MO18D04_M
C 121	22	1.7	634	12	AG016615	AG016615 Homo sapi		C 194	20	1.5	933	12	CNS0123	AL101841	Drosoph11
C 122	22	1.7	634	12	AG016615	AG016615 Homo sapi		C 195	20	1.5	953	12	B18712	B18712	F28H16-T7_I
C 123	22	1.7	639	10	W25749	W25749 11b4 Human		C 196	20	1.5	1014	12	CNS014HB	AL106745	Drosoph11
C 124	22	1.7	698	10	BE602400	BE602400 HSVME009		C 197	20	1.5	1034	12	CNS01415	AL103571	Drosoph11
C 125	22	1.7	698	12	AZ132361	AZ132361 OSMNB006		C 198	20	1.5	1101	12	CNS008M4	AL055776	Drosoph11
C 126	22	1.7	737	12	AQ328447	AQ328447 nbxb0043M		C 199	20	1.5	1101	12	CNS008M4	AL052536	Drosoph11
C 127	22	1.7	762	12	AQ330981	AQ330981 nbxb0048D		C 200	20	1.5	1101	12	CNS008M4	AL076116	Drosoph11
C 128	22	1.7	839	10	BE641285	BE641285 C112_2-NO		C 201	20	1.5	1145	12	AG185621	AG185621	Pan trogl
C 129	22	1.7	839	12	AQ751739	AQ751739 HS_5568_B		C 202	20	1.5	1325	12	AG042738	AG042738	Pan trogl
C 130	22	1.7	866	12	AQ738762	AQ738762 HS_5382_B		C 203	20	1.5	1651	12	AG086967	AG086967	Pan trogl
C 131	22	1.7	901	10	W26627	W26627 34a3 Human		C 204	20	1.5	1696	12	AG029834	AG029834	Pan trogl
C 132	22	1.7	928	12	AQ747461	AQ747461 HS_5537_A		C 205	20	1.5	1861	9	AW727919	AW727919	GA_EA002
C 133	22	1.7	986	9	BE039646	BE039646 OCO1H10_O		C 206	20	1.5	92	12	CNS00D0S	AL059779	Drosoph11
C 134	22	1.7	1101	12	CNS00H97	AL073091 Drosoph11		C 207	20	1.5	189	9	AI394822	AI394822	MA000090..
C 135	22	1.7	1129	12	AG042718	AG042718 Pan	trog1	C 208	19	1.4	302	12	CNS008BU	AL056893	Drosoph11
C 136	22	1.7	1285	10	BG857280	BG857280 T3OM24-SP6		C 209	19	1.4	304	12	CNS00A3Z	AL054896	Drosoph11
C 137	22	1.7	1321	12	AG014689	AG014689 nbdb00490		C 210	19	1.4	317	10	BMI46919	BMI46919	TCAR1E75
C 138	22	1.7	1572	12	AG150563	AG150563 Pan	trog1	C 211	19	1.4	319	12	AO235474	AO235474	HS_2050_B
C 139	22	1.7	1893	9	AW729974	AW729974 GA_EA002		C 212	19	1.4	322	12	CNS010IG	AL108967	Drosoph11
C 140	22	1.7	457	12	BH171082	BH171082 SALK_0037		C 213	19	1.4	350	12	CNS01871	AL108967	Drosoph11
C 141	22	1.6	594	10	W27268	W27268 24f3 Human		C 214	19	1.4	366	12	AO133540	AO133540	HS_3051_A
C 142	22	1.6	625	12	AQ329251	AQ329251 nbxb0044L		C 215	19	1.4	375	12	AO216167	AO216167	HS_3252_B
C 143	22	1.6	649	3	BI644982	BI644982 OP2778_M1		C 216	19	1.4	380	12	CNS0115B	AO272259	HS_5236_A
C 144	22	1.6	649	12	CNS012JM	AL101644 Drosoph11		C 217	19	1.4	382	12	AQ722593	AQ722593	SLK_0403
C 145	22	1.6	653	12	AG0051468	AG0051468 nbxb0002b		C 218	19	1.4	444	12	BH212518	BH212518	SLK_3054_B
C 146	22	1.6	712	12	AG0002802	AG0002802 Homo sapi		C 219	19	1.4	446	12	BH212518	BH212518	SLK_3054_B
C 147	22	1.6	788	9	BE040877	BE040877 OP12H12_O		C 220	19	1.4	455	12	BH213254	BH213254	SP_1021_A
C 148	22	1.6	802	3	BI644957	BI644957 OP2750_M1		C 221	19	1.4	455	12	BH213254	BH213254	SP_1021_A
C 149	22	1.6	804	3	AQ257904	AQ257904 nbxb0019C		C 222	19	1.4	455	12	BH213254	BH213254	SP_1021_A
C 150	22	1.6	892	12	CNS00CBE	AL058966 Drosoph11		C 223	19	1.4	455	12	BH213254	BH213254	SP_1021_A
C 151	22	1.6	903	10	W28594	W28594 48h7 Human		C 224	19	1.4	455	12	BH213254	BH213254	SP_1021_A
C 152	22	1.6	942	10	W28594	W28594 48h7 Human		C 225	19	1.4	455	12	BH213254	BH213254	SP_1021_A
C 153	22	1.6	987	10	BG446285	BG446285 GA_EB001		C 226	19	1.4	455	12	BH213254	BH213254	SP_1021_A
C 154	22	1.6	1040	10	BH423478	BH423478 AGENSCOURT		C 227	19	1.4	455	12	BH213254	BH213254	SP_1021_A
C 155	22	1.6	1056	12	CNS0147U	AL103812 Drosoph11		C 228	19	1.4	455	12	BH213254	BH213254	SP_1021_A
C 156	22	1.6	1095	12	BI3658	BI3658 j8b7 trypan		C 229	19	1.4	455	12	BH213254	BH213254	SP_1021_A
C 157	22	1.6	1104	12	CNS00231	AL109759 Drosoph11		C 230	19	1.4	455	12	BH213254	BH213254	SP_1021_A
C 158	22	1.6	1181	12	BI3117	BI3117 TPK3-SP6.2		C 231	19	1.4	455	12	BH213254	BH213254	SP_1021_A
C 159	22	1.6	1226	12	AG11835	AG11835 Pan	trog1	C 232	19	1.4	455	12	BH213254	BH213254	SP_1021_A
C 160	22	1.6	1326	3	BI644682	BI644682 OP2444_M1		C 233	19	1.4	455	12	BH213254	BH213254	SP_1021_A
C 161	22	1.6	2078	3	CNS00C6Z	AL058302 Drosoph11		C 234	19	1.4	455	12	BH213254	BH213254	SP_1021_A
C 162	22	1.6	2078	3	CNS00C6Z	AL058302 Drosoph11		C 235	19	1.4	455	12	BH213254	BH213254	SP_1021_A
C 163	22	1.6	2078	3	CNS00C6Z	AL058302 Drosoph11		C 236	19	1.4	455	12	BH213254	BH213254	SP_1021_A

237	19	1.4	606	12	AQ156849	AQ156849 nbxb0008F	310	18	1.4	542	10	BG485746	BG485746 NXPV_038
238	19	1.4	612	12	AQ618783	AQ618783 HS_5166_B	C 311	18	1.4	544	12	CNS01207	AL101881 Drosophill
c 239	19	1.4	629	12	CNS01337	AL103455 Drosophill	C 312	18	1.4	549	12	AZ143040	AZ143040 SP_0041_B
240	19	1.4	646	12	AG012133	AG012133 Homo sapi	C 313	18	1.4	559	12	AG090016	AG090016 nbxb0081G
241	19	1.4	680	10	BG441143	BG441143 GA_Ea001	C 314	18	1.4	563	12	CNS0173R	AL108129 Drosophill
c 242	19	1.4	710	9	AI438728	AI438728 SWOV3MCAM	C 315	18	1.4	571	12	AQ821582	AQ821582 HS_5333_A
c 243	19	1.4	714	12	AZ192040	AZ192040 SP_1020_B	C 316	18	1.4	584	10	BM341563	BM341563 MEST336-F
c 244	19	1.4	716	12	AZ184487	AZ184487 SP_1003_A	C 317	18	1.4	591	12	CNS0105D	AL098539 Drosophill
c 245	19	1.4	725	10	BE413921	BE413921 SCU004.DO	C 318	18	1.4	596	12	AQ332339	AQ332339 HS_5002_B
c 246	19	1.4	734	9	AI907080	AI907080 PM-BH1334-	C 319	18	1.4	600	10	W26715	W26715 12f3 Human
c 247	19	1.4	741	12	AQ747833	AQ747833 HS_5537_A	C 320	18	1.4	601	12	AQ783451	AQ783451 HS_3197_A
c 248	19	1.4	754	12	CNS0142A	AL103612 Drosophill	C 321	18	1.4	611	12	CNS004P4	AL054345 Drosophill
c 249	19	1.4	760	10	W28581	W28581 49f1 Human	C 322	18	1.4	613	10	BI678846	BI678846 SWS744 SW
c 250	19	1.4	771	3	BI645302	BI645302 OP2042 M1	C 323	18	1.4	613	10	W27439	W27439 31g1 Human
c 251	19	1.4	776	10	W22072	W22072 61B8 Human	C 324	18	1.4	614	12	CNS010B2	AL098744 Drosophill
c 252	19	1.4	777	12	AQ325246	AQ325246 mgxb0021M	C 325	18	1.4	615	12	CNS010G2	AL098924 Drosophill
c 253	19	1.4	788	12	AG117202	AG117202 Pan trogl	C 326	18	1.4	624	12	AQ664612	AQ664612 HS_5234_A
254	19	1.4	808	12	CNS0136A	AL102460 Drosophill	C 327	18	1.4	628	12	AQ802195	AQ802195 HS_3167_B
255	19	1.4	827	12	AQ749110	AQ749110 HS_5338_A	C 328	18	1.4	640	10	BM337503	BM337503 MEST207-G
256	19	1.4	828	12	AQ742965	AQ742965 HS_5386_B	C 329	18	1.4	640	10	BM349594	BM349594 MEST252-D
c 257	19	1.4	829	10	W28069	W28069 44f3 Human	C 330	18	1.4	649	12	AZ178369	AZ178369 SP_0161_A
c 258	19	1.4	840	12	AZ188428	AZ188428 SP_1012_A	C 331	18	1.4	650	10	BF297383	BF297383 051PBA11
c 259	19	1.4	864	10	W28494	W28494 47h12 Human	C 332	18	1.4	652	9	AW956585	AW956585 EST368670
c 260	19	1.4	883	10	BF607122	BF607122 MFL_00006	C 333	18	1.4	652	12	AQ515657	AQ515657 HS_5237_A
c 261	19	1.4	891	9	AI605948	AI605948 mu41g11.Y	C 334	18	1.4	654	12	AQ561467	AQ561467 HS_5189_B
c 262	19	1.4	917	12	AG160672	AG160672 Pan trogl	C 335	18	1.4	663	10	BM336005	BM336005 MEST186-A
c 263	19	1.4	980	12	AG076025	AG076025 Pan trogl	C 336	18	1.4	664	12	CNS013JK	AL102938 Drosophill
c 264	19	1.4	988	12	CNS013VK	AL102074 Drosophill	C 337	18	1.4	668	12	AQ725569	AQ725569 HS_5394_A
c 265	19	1.4	1050	10	BI180678	BI180678 LRH20G8_L	C 338	18	1.4	670	12	AG016061	AG016061 Homo sapi
c 266	19	1.4	1058	10	BM423394	BM423394 AGENCOURT	C 339	18	1.4	675	10	BI886875	BI886875 2F637-1-0
c 267	19	1.4	1101	12	CNS0082W	AL052948 Drosophill	C 340	18	1.4	677	12	AQ324718	AQ324718 mgxb0019J
c 268	19	1.4	1101	12	CNS0082W	AL052948 Drosophill	C 341	18	1.4	682	10	W27604	W27604 35b1 Human
c 269	19	1.4	1101	12	CNS0082W	AL052948 Drosophill	C 342	18	1.4	684	10	W27140	W27140 24g11 Human
c 270	19	1.4	1101	12	CNS0082W	AL052948 Drosophill	C 343	18	1.4	688	10	BM337303	BM337303 MEST205-H
c 271	19	1.4	1111	12	CNS017QV	AL083835 Drosophill	C 344	18	1.4	696	10	BF865341	BF865341 963058H11
c 272	19	1.4	1164	10	BE422124	BE422124 HMB0200C	C 345	18	1.4	704	12	BI0025	BI0025 T3F24-Sp6 T
c 273	19	1.4	1203	10	BE427878	BE427878 PSR6884_I	C 346	18	1.4	704	12	AG013874	AG013874 Homo sapi
c 274	19	1.4	1491	12	AG172774	AG172774 Pan trogl	C 347	18	1.4	704	12	AG090382	AG090382 Pan trogl
c 275	19	1.4	1700	3	BI644765	BI644765 OP2259 M1	C 348	18	1.4	707	12	BI9588	BI9588 T2203-T7.1
c 276	19	1.4	1791	12	AG056213	AG056213 Pan trogl	C 349	18	1.4	707	12	AG012499	AG012499 Homo sapi
c 277	18	1.4	33	12	CNS0082R	AL056350 Drosophill	C 350	18	1.4	708	12	BI9526	BI9526 F20116-T7.1
c 278	18	1.4	102	12	CNS008H28	AL072840 Drosophill	C 351	18	1.4	718	10	BM348669	BM348669 MEST294-E
c 279	18	1.4	130	12	CNS00HV1	AL074079 Drosophill	C 352	18	1.4	722	10	W27620	W27620 35c8 Human
c 280	18	1.4	154	12	CNS014WM	AL104704 Drosophill	C 353	18	1.4	737	12	AG098331	AG098331 Pan trogl
c 281	18	1.4	234	9	AV919220	AV919220 AV919220	C 354	18	1.4	738	10	BM350624	BM350624 MEST211-B
c 282	18	1.4	279	12	CNS002Y1	AL098292 Drosophill	C 355	18	1.4	738	10	W25801	W25801 13f3 Human
c 283	18	1.4	299	12	CNS07H03	AL610437 Anopheles	C 356	18	1.4	739	10	W25909	W25909 14g9 Human
c 284	18	1.4	322	12	BH610817	BH610817 SALK_0180	C 357	18	1.4	742	10	BM332671	BM332671 MEST176-A
c 285	18	1.4	339	12	BH616955	BH616955 SALK_0357	C 358	18	1.4	751	12	AG008138	AG008138 Homo sapi
c 286	18	1.4	342	9	AI752889	AI752889 cr01h01.X	C 359	18	1.4	752	12	AG179858	AG179858 Pan trogl
c 287	18	1.4	351	12	CNS008KT	AL071910 Drosophill	C 360	18	1.4	756	12	CNS009KH	AL033790 Drosophill
c 288	18	1.4	355	12	CNS004GW	AL078480 Drosophill	C 361	18	1.4	758	10	W28084	W28084 41g8 Human
c 289	18	1.4	356	10	BI784123	BI784123 kh31b03.Y	C 362	18	1.4	762	10	AQ896736	AQ896736 HS_3153_A
c 290	18	1.4	383	12	CNS003CX	AL076019 Drosophill	C 363	18	1.4	763	12	AG047248	AG047248 Pan trogl
c 291	18	1.4	385	10	BM350294	BM350294 MEST263-G	C 364	18	1.4	764	12	AG060281	AG060281 Drosophill
c 292	18	1.4	387	9	AW958489	AW958489 EST370559	C 365	18	1.4	764	3	BI645311	BI645311 OP2138 M1
c 293	18	1.4	390	12	CNS0066E	AL062851 Drosophill	C 366	18	1.4	779	12	BI8684	BI8684 F23C5-T7.1
c 294	18	1.4	397	10	BI747179	BI747179 km36h03.Y	C 367	18	1.4	788	10	BM480308	BM480308 AGENCOURT
c 295	18	1.4	434	12	BH250915	BH250915 SALK_0107	C 368	18	1.4	790	10	BF066045	BF066045 HV_CEB001
c 296	18	1.4	438	12	AZ152507	AZ152507 SP_0028_A	C 369	18	1.4	792	10	BM393076	BM393076 50071-2-5
c 297	18	1.4	442	12	BH213314	BH213314 SALK_0090	C 370	18	1.4	792	10	BM393464	BM393464 50073-2-5
c 298	18	1.4	456	10	BG520374	BG520374 ps20q04.Y	C 371	18	1.4	808	10	BE421799	BE421799 HMB014CG
c 299	18	1.4	458	12	AZ161436	AZ161436 SP_0069_B	C 372	18	1.4	814	12	AZ198861	AZ198861 SP_1038_B
c 300	18	1.4	463	12	BH611836	BH611836 SALK_0317	C 373	18	1.4	816	12	AQ863301	AQ863301 nbe0020P
c 301	18	1.4	467	12	BH212559	BH212559 SALK_0077	C 374	18	1.4	822	12	AQ749552	AQ749552 HS_5575_A
c 302	18	1.4	471	10	W27334	W27334 27f12 Human	C 375	18	1.4	823	12	CNS0105K	AL098546 Drosophill
c 303	18	1.4	485	12	CNS00020	AL097122 Drosophill	C 376	18	1.4	825	12	AZ196113	AZ196113 SP_1031_A
c 304	18	1.4	498	12	BH172709	BH172709 SALK_0060	C 377	18	1.4	826	12	CNS0132C	AL102318 Drosophill
c 305	18	1.4	518	9	AL523777	AL523777 AL523777	C 378	18	1.4	839	12	AQ751739	AQ751739 HS_5568_B
c 306	18	1.4	518	12	AQ465238	AQ465238 HS_5072_B	C 379	18	1.4	844	12	AQ746350	AQ746350 HS_2277-A
c 307	18	1.4	532	10	BM349263	BM349263 MEST246-G	C 380	18	1.4	861	12	B20940	B20940 T6B15-T7 TA
c 308	18	1.4	540	10	BM074692	BM074692 MEST296-D	C 381	18	1.4	862	12	CNS013MG	AL103042 Drosophill
c 309	18	1.4	540	12	AZ145010	AZ145010 SP_0019_B	C 382	18	1.4				

C 383	18	1.4	864	12	AG175870	AG175870 Pan trogl	C 456	17	1.3	200	12	CNS0039C	AL063917 Drosophill
C 384	18	1.4	869	12	CNS002EK	AL097574 Drosophill	C 457	17	1.3	202	12	CNS010TO	AL099416 Drosophill
C 385	18	1.4	870	12	AQ741290	AQ741290 HS_5534-A	C 458	17	1.3	207	12	CNS013L3	AL102993 Drosophill
C 386	18	1.4	874	12	B10287	B10287 T12C8-T7 TA	C 459	17	1.3	210	12	CNS011AM	AL100034 Drosophill
C 387	18	1.4	881	12	W26682	W26682 34d6 Human	C 460	17	1.3	215	9	AW156842	AW156842 se31e08.y
C 388	18	1.4	884	12	CNS01259	AL101137 Drosophill	C 461	17	1.3	239	10	BM092012	BM092012 seah06063
C 389	18	1.4	885	12	W26628	W26628 34d4 Human	C 462	17	1.3	252	12	BM618025	BM618025 SALK_0383
C 390	18	1.4	885	12	CNS012GX	AL101348 Drosophill	C 463	17	1.3	261	12	CNS00FR2	AL071175 Drosophill
C 391	18	1.4	886	12	AQ749812	AQ749812 HS_5573-A	C 464	17	1.3	263	9	BE058741	BE058741 sn20c01.y
C 392	18	1.4	890	3	B1644464	B1644464 OP2191 M1	C 465	17	1.3	273	12	BH253165	BH253165 SALK_0145
C 393	18	1.4	895	12	AZ198010	AZ198010 SE_1036-B	C 466	17	1.3	276	12	BM634199	BM634199 SALK_0448
C 394	18	1.4	920	9	AT438725	AT438725 SMOV3MCM	C 467	17	1.3	284	10	B1783357	B1783357 k118h02.Y
C 395	18	1.4	922	12	CNS00ZOG	AL098002 Drosophill	C 468	17	1.3	285	9	AW974475	AW974475 EST386579
C 396	18	1.4	926	12	B10413	B10413 P2615-SP6 I	C 469	17	1.3	285	12	CNS00G01	AW974475 Drosophill
C 397	18	1.4	928	12	B09063	B09063 F20P19-SP6	C 470	17	1.3	287	9	AW132190	AW132190 sd67d02.Y
C 398	18	1.4	932	12	AQ747290	AQ747290 HS_5537-A	C 471	17	1.3	291	12	AQ066489	AQ066489 HS_2247-A
C 399	18	1.4	934	12	B12492	B12492 F17P6-SP6 I	C 472	17	1.3	294	10	B1945129	B1945129 sb26c10.Y
C 400	18	1.4	945	12	CNS0549S	AL320473 Tetradon	C 473	17	1.3	296	10	BE597977	BE597977 su89h05.Y
C 401	18	1.4	959	12	CNS05GCG	AL336107 Tetradon	C 474	17	1.3	296	12	BH213829	BH213829 SALK_0097
C 402	18	1.4	966	10	W28562	W28562 48g11 Human	C 475	17	1.3	305	10	B1498003	B1498003 sag30g10.
C 403	18	1.4	969	10	W08324	W08324 mb40g10.r1	C 476	17	1.3	307	12	CNS012IP	AL101611 Drosophill
C 404	18	1.4	988	10	W26659	W26659 34d2 Human	C 477	17	1.3	309	12	BH613962	BH613962 SALK_0352
C 405	18	1.4	997	12	CNS005TE	AL060767 Drosophill	C 478	17	1.3	310	12	BH617007	BH617007 SALK_0358
C 406	18	1.4	1009	12	AG134488	AG134488 Pan trogl	C 479	17	1.3	312	10	B1742891	B1742891 SALK_0097
C 407	18	1.4	1020	10	BM415405	BM415405 OP20479 M	C 480	17	1.3	318	10	B1020356	B1020356 SALK_0135
C 408	18	1.4	1027	10	BM463476	BM463476 AGENCCOURT	C 481	17	1.3	318	12	BH252532	BH252532 SALK_0135
C 409	18	1.4	1033	12	AG136543	AG136543 Pan trogl	C 482	17	1.3	330	10	BM424272	BM424272 fw44d07.Y
C 410	18	1.4	1041	12	CNS057PR	AL324936 Tetradon	C 483	17	1.3	332	12	CNS013OX	AL103203 Drosophill
C 411	18	1.4	1042	10	BE427789	BE427789 PSR6749 I	C 484	17	1.3	334	12	CNS010XL	AL099555 Drosophill
C 412	18	1.4	1057	9	AI581449	AI581449 SMOV3MCM	C 485	17	1.3	336	12	AQ094010	AQ094010 HS_2199-A
C 413	18	1.4	1057	9	AG161620	AG161620 Pan trogl	C 486	17	1.3	338	9	AA214964	AA214964 mu83a06.x
C 414	18	1.4	1058	12	CNS05L6K	AL342389 Tetradon	C 487	17	1.3	339	12	CNS00ZE6	AL097560 Drosophill
C 415	18	1.4	1073	12	AG101312	AG101312 Pan trogl	C 488	17	1.3	341	10	B1781919	B1781919 k103a09.Y
C 416	18	1.4	1094	10	BM458870	BM458870 AGENCCOURT	C 489	17	1.3	346	12	AG171212	AG171212 Pan trogl
C 417	18	1.4	1101	10	BM4771102	BM4771102 AGENCCOURT	C 490	17	1.3	347	9	AW069964	AW069964 mg1e1002B
C 418	18	1.4	1101	12	CNS00GCG	AL1072174 Drosophill	C 491	17	1.3	348	10	B1427247	B1427247 sah78a09.Y
C 419	18	1.4	1101	12	CNS016WC	AL107288 Drosophill	C 492	17	1.3	349	12	AI736154	AI736154 sb23h04.Y
C 420	18	1.4	1101	12	CNS016WC	AL107288 Drosophill	C 493	17	1.3	351	12	CNS07FAP	AL068222 Anopheles
C 421	18	1.4	1107	9	AI381159	AI381159 SMOV1CAR	C 494	17	1.3	351	10	BM025809	BM025809 f583f01.Y
C 422	18	1.4	1178	12	BE420639	BE420639 HMM001.AO	C 495	17	1.3	358	9	AW077052	AW077052 fj04c01.Y
C 423	18	1.4	1257	12	AG014678	AG014678 nbe0049M	C 496	17	1.3	358	12	AQ300005	AQ300005 HS_3076-B
C 424	18	1.4	1257	12	AG132022	AG132022 Pan trogl	C 497	17	1.3	362	10	BE437779	BE437779 T076d01.x
C 425	18	1.4	1283	10	BM4773476	BM4773476 AGENCCOURT	C 498	17	1.3	363	12	CNS00UCB	AL067936 Drosophill
C 426	18	1.4	1376	12	AG078968	AG078968 HS_3154-A	C 499	17	1.3	363	10	BE247486	BE247486 TCBRPIR64
C 427	18	1.4	1533	12	AG030232	AG030232 Pan trogl	C 500	17	1.3	368	12	CNS00DHR	AL076248 Drosophill
C 428	18	1.4	1588	12	AG029906	AG029906 Pan trogl	C 501	17	1.3	368	10	B1939099	B1939099 daa82e01.
C 429	18	1.4	1877	3	BI644353	BI644353 OP2072 M1	C 502	17	1.3	369	12	AQ137700	AQ137700 HS_3065-B
C 430	18	1.4	1926	12	AG123346	AG123346 Pan trogl	C 503	17	1.3	371	9	AW953318	AW953318 EST365388
C 431	18	1.4	1966	9	AW730391	AW730391 GA_Ea002	C 504	17	1.3	372	12	AQ090902	AQ090902 HS_3009-B
C 432	18	1.4	1966	12	AG055545	AG055545 Pan trogl	C 505	17	1.3	374	10	B1703216	B1703216 f545e04.Y
C 433	18	1.4	2033	12	AG120692	AG120692 Pan trogl	C 506	17	1.3	375	12	CNS00G16	AL072219 Drosophill
C 434	18	1.4	2070	3	BI644728	BI644728 OP2492 M1	C 507	17	1.3	377	10	BI945168	BI945168 AL363168
C 435	18	1.4	2149	12	AG170973	AG170973 Pan trogl	C 508	17	1.3	377	10	BI945168	BI945168 sc46h11.Y
C 436	18	1.4	2312	9	BE054816	BE054816 GA_Ea003	C 509	17	1.3	387	10	BM356370	BM356370 kx63f03.Y
C 437	18	1.4	2464	12	AG030682	AG030682 Pan trogl	C 510	17	1.3	389	10	BM026161	BM026161 fu75d05.Y
C 438	18	1.4	2509	9	AW730170	AW730170 GA_Ea000	C 511	17	1.3	394	10	B1749172	B1749172 ro74g08.Y
C 439	18	1.4	2946	12	AG053805	AG053805 Pan trogl	C 512	17	1.3	395	12	CNS02ICB	AL198740 Tetradon
C 440	18	1.4	3416	10	BM415288	BM415288 OP20360 M	C 513	17	1.3	398	9	AW990457	AW990457 uf37c06.Y
C 441	18	1.4	3416	10	BM415288	BM415288 OP20360 M	C 514	17	1.3	399	10	BE286577	BE286577 039pBa03
C 442	17	1.3	77	12	CNS00DBH	AL052178 Drosophill	C 515	17	1.3	402	9	AW733830	AW733830 sk788d02.Y
C 443	17	1.3	77	12	CNS00DBH	AL052178 Drosophill	C 516	17	1.3	405	10	BM026415	BM026415 f07f06.Y
C 444	17	1.3	88	9	AI522632	AI522632 f660f02.x	C 517	17	1.3	405	10	BM086837	BM086837 H315G05-
C 445	17	1.3	88	9	AI522632	AI522632 f660f02.x	C 518	17	1.3	405	10	BM186146	BM186146 fV98e04.Y
C 446	17	1.3	92	12	CNS00CXS	AL058785 Drosophill	C 519	17	1.3	409	9	AW762642	AW762642 ur64g11.Y
C 447	17	1.3	94	12	CNS00BXY	AL052116 Drosophill	C 520	17	1.3	409	10	BM310541	BM310541 SMOV3MCM
C 448	17	1.3	95	12	CNS00BXY	AL052116 Drosophill	C 521	17	1.3	411	12	BM619290	BM619290 SALK_0407
C 449	17	1.3	103	12	CNS00BXY	AL052116 Drosophill	C 522	17	1.3	415	12	CNS00AK2	AL055576 Drosophill
C 450	17	1.3	125	10	BE241434	BE241434 TCAPLID0	C 523	17	1.3	419	12	BI527572	BI527572 102d08260
C 451	17	1.3	139	10	BJ139287	BJ139287 RJ139287	C 524	17	1.3	425	12	BM633713	BM633713 SALK_0430
C 452	17	1.3	162	12	CNS016CK	AL106767 Drosophill	C 525	17	1.3	427	9	AT152954	AT152954 ct02g06.x
C 453	17	1.3	176	12	BM610869	BM610869 SALK_0181	C 526	17	1.3	427	10	BM070287	BM070287 l080c03.Y
C 454	17	1.3	197	10	BG520397	BG520397 ps13h11.Y	C 527	17	1.3	429	12	BM616939	BM616939 SALK_0356
C 455	17	1.3	199	12	CNS07HNG	AL611278 Anopheles	C 528	17	1.3	429	12	BM634254	BM634254 SALK_0450

c 529	17	1.3	431	12	AQ182510	HS_3074_B	AL067475	Drosophil
c 530	17	1.3	433	10	BI840396	fs73d06.Y	AQ330634	nbxb0047L
c 531	17	1.3	433	12	AZ147885	SP_0011_B	AQ609626	HS_5079_A
c 532	17	1.3	435	10	BM129014	lf16d07.Y	BG578326	df18a10.Y
c 533	17	1.3	436	10	BF151169	uz06a06.Y	AQ556610	HS_5232_A
c 534	17	1.3	436	12	BH254926	SA_LK_0174	AQ892310	HS_2025_B
c 535	17	1.3	436	12	FR0005325		AZ180989	SP_0183_A
c 536	17	1.3	437	10	BI440845		BG418255	HVSMK002
c 537	17	1.3	437	12	BH213365	ic77b11.Y	BM473078	AGENCOURT
c 538	17	1.3	444	10	BI703319	fs84d12.Y	BI787001	sal58a02
c 539	17	1.3	444	12	AZ132682	OSJNB010	AZ34959	HS_5126_B
c 540	17	1.3	445	10	BI889056	2F637-2-0	W27395	28d8 Human
c 541	17	1.3	445	10	BE301345	bd05h08.X	W27395	28d8 Human
c 542	17	1.3	448	12	BH171368	SA_LK_0041	AL059282	Drosophil
c 543	17	1.3	455	12	BH633738	SA_LK_0431	AZ182432	SP_0189_A
c 544	17	1.3	456	9	AW734897	SK76d08.Y	AL05455	Drosophil
c 545	17	1.3	456	10	W26410	29c11 Human	AL098335	Drosophil
c 546	17	1.3	457	12	AQ866395	nbe0028A	BE223097	988S0133
c 547	17	1.3	460	12	AQ856784		AL068968	Drosophil
c 548	17	1.3	461	9	AW913273		BH126359	BARC-Satt
c 549	17	1.3	463	9	AW020936	uf51b02.Y	AW958697	EST370767
c 550	17	1.3	464	12	AQ862770	nbe00019D	W27392	28d3 Human
c 551	17	1.3	466	10	BF278215	GA_Eb003	AL102815	Drosophil
c 552	17	1.3	467	12	BH211812	SALK_0066	BE223053	hu46f01.X
c 553	17	1.3	469	10	BM092963	sa103c04	AQ804564	HS_3025_A
c 554	17	1.3	471	9	AI877750	fc51b10.Y	AZ175115	HS_5436_A
c 555	17	1.3	474	12	CNS00040		BF272787	GA_EB001
c 556	17	1.3	476	9	AW963655		AW959279	EST371349
c 557	17	1.3	478	12	AG161519	Pan trogl	AQ465562	HS_5121_B
c 558	17	1.3	479	12	CNS00CYB		W28332	45d6 Human
c 559	17	1.3	480	12	AZ159198	SP_0062_A	AZ179384	SP_0165_A
c 560	17	1.3	481	9	BI135194	ug28b05.Y	AQ694801	HS_5486_A
c 561	17	1.3	483	10	HI15528	ym37b01.sl	AQ350458	GM210008B
c 562	17	1.3	484	12	HI15550	ym27e01.sl	AW350458	GM210008B
c 563	17	1.3	484	12	AZ145096		W27342	27g11 Human
c 564	17	1.3	488	12	AQ880112	HS_4868_B	W26675	11b11 Human
c 565	17	1.3	490	12	CNS016W4		W28054	41f1 Human
c 566	17	1.3	490	12	AQ495110	HS_5203_A	AQ618898	HS_5177_B
c 567	17	1.3	492	12	CNS01006		AQ801475	HS_5396_A
c 568	17	1.3	492	12	CNS0101D		AQ576677	nbxb0089J
c 569	17	1.3	493	12	BG656882		W27059	20a1 Human
c 570	17	1.3	495	12	AQ495102	HS_5203_A	AQ618620	HS_5173_B
c 571	17	1.3	497	10	BG551859		W27269	24f4 Human
c 572	17	1.3	497	10	BF195373	7n17a03.X	W28158	42g7 Human
c 573	17	1.3	500	10	BI886529	2F637-1-0	AZ170493	SP_0116_B
c 574	17	1.3	501	10	BM336016	MEST186-B	AL098308	Drosophil
c 575	17	1.3	502	12	AQ189277	HS_3205_B	AL098308	Drosophil
c 576	17	1.3	504	12	AZ162996	SP_0073_A	W27796	37g8 Human
c 577	17	1.3	505	10	BE849741	uw18b02.Y	AQ143800	HS_3075_B
c 578	17	1.3	507	10	BM129173	1f18a02.Y	W27796	37g8 Human
c 579	17	1.3	511	10	BJ099199	BU093199	W27796	37g8 Human
c 580	17	1.3	511	12	AQ206838		W27796	37g8 Human
c 581	17	1.3	519	9	AW726955		W27796	37g8 Human
c 582	17	1.3	522	12	AZ024319	RFC1-23-3	W27796	37g8 Human
c 583	17	1.3	522	12	AZ154546	SP_0051_B	W27796	37g8 Human
c 584	17	1.3	524	12	AQ560520	HS_2082_B	W27796	37g8 Human
c 585	17	1.3	525	12	AQ804872	HS_3185_A	W27796	37g8 Human
c 586	17	1.3	526	12	AQ808364	HS_4508_B	W27796	37g8 Human
c 587	17	1.3	528	12	AQ710433	HS_5378_B	W27796	37g8 Human
c 588	17	1.3	529	9	AA495552		W27796	37g8 Human
c 589	17	1.3	536	9	BE040428	OE06A03 O	W27796	37g8 Human
c 590	17	1.3	536	12	AQ441815		W27796	37g8 Human
c 591	17	1.3	540	9	AW968981	EST381058	W27796	37g8 Human
c 592	17	1.3	540	9	AA495533		W27796	37g8 Human
c 593	17	1.3	540	12	AZ155767	SP_0044_A	W27796	37g8 Human
c 594	17	1.3	542	10	BI202841	NXPV_091	W27796	37g8 Human
c 595	17	1.3	543	10	BE690060	uw63h01.Y	W27796	37g8 Human
c 596	17	1.3	544	12	AQ768028	HS_3189_A	W27796	37g8 Human
c 597	17	1.3	547	10	BI900336	ld11f09.Y	W27796	37g8 Human
c 598	17	1.3	550	12	AG047371	Pan trogl	W27796	37g8 Human
c 599	17	1.3	551	12	AZ154656	SP_0045_A	W27796	37g8 Human
c 600	17	1.3	551	12	AQ303677	HS_3200_B	W27796	37g8 Human
c 601	17	1.3	553	10	BI888812	2F637-2-0	W27796	37g8 Human

C 675	17	1.3	641	12	AQ510128	AQ510128 nbxb0094H	C 748	17	1.3	727	10	W25918	W25918 14h7 Human
C 676	17	1.3	647	10	B1352769	B1352769 pppIn.pk0	C 749	17	1.3	730	12	AG184885	AG184885 Pan trogl
C 677	17	1.3	647	10	W27033	W27033 19d9 Human	C 750	17	1.3	731	12	AZ200484	AZ200484 SP_1025_A
C 678	17	1.3	647	10	W27819	W27819 38b9 Human	C 751	17	1.3	732	10	W26017	W26017 18b6 Human
C 679	17	1.3	647	12	B10659	B10659 F14O3-r7 IG	C 752	17	1.3	732	12	AG012520	AG012520 Homo sapi
C 680	17	1.3	649	10	W27563	W27563 34g10 Human	C 753	17	1.3	733	12	AG163895	AG163895 Pan trogl
C 681	17	1.3	650	10	BE427593	BE427593 PSR7237 I	C 754	17	1.3	734	12	AG174008	AG174008 Pan trogl
C 682	17	1.3	650	10	BE427606	BE427606 PSR7251 I	C 755	17	1.3	735	12	AG173962	AG173962 Pan trogl
C 683	17	1.3	650	10	BE427611	BE427611 PSR7339 I	C 756	17	1.3	736	12	AG126221	AG126221 Pan trogl
C 684	17	1.3	650	10	BE427682	BE427682 PSR7339 I	C 757	17	1.3	736	12	CNS00DMC	CNS00DMC
C 685	17	1.3	652	12	AG015473	AG015473 Homo sapi	C 758	17	1.3	739	12	AZ199789	AZ199789 SP_1040_B
C 686	17	1.3	653	9	AW963003	AW963003 EST375076	C 759	17	1.3	740	10	B1887634	B1887634
C 687	17	1.3	653	12	AZ183514	AZ183514 HS_1001_A	C 760	17	1.3	740	12	AQ331048	AQ331048 nbxb0048L
C 688	17	1.3	654	12	AQ562219	AQ562219 HS_5234_A	C 761	17	1.3	742	10	W26711	W26711 13e3 Human
C 689	17	1.3	656	10	BM268277	BM268277 MEST379-H	C 762	17	1.3	744	12	AZ192534	AZ192534 SP_1021_B
C 690	17	1.3	656	10	BF297428	BF297428 051PBF03	C 763	17	1.3	744	12	AG001227	AG001227 Homo sapi
C 691	17	1.3	656	12	AG085349	AG085349 Pan trogl	C 764	17	1.3	744	12	AG090934	AG090934 Pan trogl
C 692	17	1.3	658	10	W27617	W27617 35c5 Human	C 765	17	1.3	745	12	B21442	B21442 T13F1-T7 TA
C 693	17	1.3	662	10	BM158630	BM158630 NXLV_037	C 766	17	1.3	746	12	AQ273343	AQ273343 nbxb0029H
C 694	17	1.3	662	12	AG012151	AG012151 Homo sapi	C 767	17	1.3	749	12	AQ745752	AQ745752 HS_2272_A
C 695	17	1.3	664	10	W22078	W22078 61C6 Human	C 768	17	1.3	749	12	AZ190837	AZ190837 SP_1018_A
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C 994	17	1.3	1098	12	AG107652	AG107652 Pan trogl
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ALIGNMENTS

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AUTHORS	Ekhavota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
TITLE	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;				
JOURNAL	Birthrididae; Oryzeae; Oryza.				
COMMENT	1 (bases 1 to 698)				
	Wing, R.A. and Dean, R.A.				
	A BAC End Sequencing Framework to Sequence the Rice Genome				
	Unpublished (1998)				
	Contact: Wing RA				
	Clemson University Genomics Institute				
	Clemson University				
	100 Jordan Hall, Clemson, SC 29634, USA				
	Tel: 864 656 7288				
	Fax: 864 656 4293				
	Email: rwing@clemson.edu				
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	Class: BAC ends				
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 HindIII; Rice is one of two most popular grains in the
 world. Half of the world population especially those
 inhabiting highly populated areas of the humid tropics
 and subtropics, rely on rice as their primary source of
 carbohydrate. Monocotyledonous rice is a diploid plant
 (2n=24) with a haploid genome equivalent of 431 Mbp
 (Arumuganathan and Earle, 1991). The relatively small
 genome of rice, three times larger than that of
 Arabidopsis, makes it suitable for genomic studies. In
 order to facilitate positional cloning, physical mapping
 and genome sequencing of rice, we have constructed a BAC
 library from Oryza sativa, Nipprobare variety. The
 library contains 36,864 clones with an average insert size
 of 128.5 kb providing 10.9 haploid genome equivalents. The
 deep coverage allows the isolation a particular sequence
 with a probability of 99.9 %. Two high density filters,
 each containing 18,432 clones (doubly spotted), represent
 the whole library for colony screening."

[illegible]

<p>AL186959</p> <p>LOCUS</p> <p>DEFINITION</p> <p>ACCESSION</p> <p>VERSION</p> <p>KEYWORDS</p> <p>SOURCE</p> <p>ORGANISM</p> <p>REFERENCE</p> <p>AUTHORS</p> <p>TITLE</p> <p>JOURNAL</p> <p>MEDLINE</p> <p>COMMENT</p> <p>FEATURES</p> <p>SOURCE</p>	<p>778 bp DNA linear GSS 30-ANG-2000</p> <p>SP_1008_A2.A03_T7A Strongylocentrotus purpuratus, purple sea urchin , sperm genomic BAC library strongylocentrotus purpuratus genomic clone plate-1008 Col-6 Row-A, DNA sequence.</p> <p>AZ186959</p> <p>AZ186959.1. GI:8370137</p> <p>GSS.</p> <p>Strongylocentrotus purpuratus. Strongylocentrotus purpuratus. Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa; Echinoidea; Euechinoidea; Echinacea; Echinoidea; Strongylocentroloidae; Strongylocentrotus. 1 (bases 1 to 778) Cameron,R.A., Mahiras,G., Rast,J.P., Martinez,P., Blondi,T.R., Swartzell,S., Wallace,J.C., Pouzbek,A.J., Livingston,B.T., Wray ,G.A., Ettensohn,C.A., Lehrach,H., Britten,R.J., Davidson,E.H. and Hood,L. A sea urchin genome project: Sequence scan, virtual map, and additional resources Proc. Natl. Acad. Sci. U. S. A. 97 (17), 9514-9518 (2000)</p> <p>20402566</p> <p>Contact: Cameron, RA, Davidson, EH, Hood, L Division of Biology 156-29 California Institute of Technology Pasadena California 91125, USA Tel: (626) 395-8421 Fax: (626) 793-3047 Email: acameron@caltech.edu Plate: 1008 row: A column: 6 Seg primer: T7 Class: BAC ends High quality sequence stop: 778.</p> <p>1..778 location/Qualifiers /organism="Strongylocentrotus purpuratus" /db_xref="taxon:7668"</p>
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AUTHORS	1 (bases 1 to 489) Cameron,R.A., Mahairas,G., Rast,J.P., Martinez,P., Biondi,T.R., Swartzell,S., Wallace,J.C., Poultke,A.J., Livingston,B.T., Wray,G.A., Ettensohn,C.A., Lehrach,H., Britten,R.J., Davidson,E.H. and Hood,L.					
TITLE	A sea urchin genome project: Sequence scan, virtual map, and additional resources					
JOURNAL	Proc. Natl. Acad. Sci. U. S. A. 97 (17), 9514-9518 (2000)					
MEDLINE	20402566					
COMMENT	Contact: Cameron, RA, Davidson, EH, Hood, L Division of Biology 156-28 California Institute of Technology Pasadena California 91125, USA Tel: (626) 395-8421 Fax: (626) 793-1047 Email: acameron@caltech.edu Plate: 82 row: C column: 8 Seq primer: T7 Class: BAC ends High quality sequence stop: 489. Location/Qualifiers 1. 489					
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AUTHORS	1 (bases 1 to 558) Wing,R.A. and Dean,R.A.					
TITLE	A BAC End Sequencing Framework for the Rice Genome					
JOURNAL	Unpublished (1998)					
COMMENT	Contact: Wing RA Clemson University Genomics Institute					

```

Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7298
Fax: 864 656 4293
Email: twing@clemson.edu
Seq primer: TAATACGACCTCATTAGGC
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            /vector="peloBAC11; Site_1: HindIII; Site_2: HindIII; Rice is one of two most popular grains in the world. Half of the world population especially those inhabiting highly populated areas of the humid tropics and subtropics, rely on rice as their primary source of carbohydrate. Monocytledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mbp (Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Nipponbare variety. The library contains 36,864 clones with an average insert size of 128.5 Kb providing 10.9 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Two high density filters, each containing 18 432 clones (doubly spotted), represent the whole library for colony screening."
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VERSION W27482.1 GI:1307286
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
Mol. Cell. Biol. 14(1):1-11 (1994)
Macke, J., Smallwood, P. and Nathans, J.
Adult Human Retina cDNA
Unpublished (1996)
Contact: Dr. Jeremy Nathans
Dr. Jeremy Nathans, Dept. of Molecular Biology and Genetics
Johns Hopkins School of Medicine
725 North Wolfe Street, Baltimore, MD 21205
Tel: 410 955 4678
Fax: 410 614 0827
Email: jeremy_nathans@gmail.bs.jhu.edu

```



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OY 1283 nnnnnnnnnnnnnnnnnnnnnnnnn 1306
LOCUS 11
DEFINITION
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JOURNAL
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Drosophila melanogaster genome survey sequence TET3 end of BAC #
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fly), genomic survey sequence.
AL054511
AL054511.1 GI:4935684
GSS
fruit fly.
Drosophila melanogaster
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 326)
Genoscope.
Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :

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COMMENT

- Web : www.genoscope.cns.fr
BP 191 91006 Evry cedex - FRANCE (E-mail : segref@genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACS. For further information please see <http://www.fruitfly.org>. The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mamoser at Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPcI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's p1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPac Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

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Oy 1279 nnaannnnnnnnnnnnnnnnn 1302
|||||
Db 181 NNNNANNNNNNNNNNNNNNNNNN 158

RESULT 12

BM270207 337 bp mRNA linear EST 20-DEC-2001
LOCUS sak25t01.y1 gm-cl075 glycine max cdna clone SOYBEAN CLONE ID:
gm-cl075-4201 5 , mRNA sequence.

ACCSSION BM270207
VERSION BM270207.1 GI:17963458
KEYWORDS EST.
SOURCE soybean.
ORGANISM Glycine max
Embryoto: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 337)
Shoenmaker,R., Keim,P., Vodkin,L., Erpelting,J., Coryell,V., Khanna,
A., Bolia,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
Wylie,T., Underwood,K., Stepien,M., Thelsing,D., Allen,M., Bowers
X,Y., Person.B., Swaller,T., Gibbons.M., Page.D., Harvey,N., Schurk
R., Ritter,E., Korn,S., Shin,T., Jackson,X., Cardenas,M., McCann
R., Waterston.R. and Wilson.R.
Public Soybean EST project
Unpublished (1999)
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Fax: 314 286 1800
Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact: ccutresgen.com web site:
www.resgen.com
Putative full length read
vector to vector length is 338

* .

3448967 BIOSIS NO.: 200200077788

Consensus PCR and microarray for diagnosis of the genus

Staphylococcus, species, and methicillin resistance.

AUTHOR: Hamels S(a); Gala J-L; Dufour S; Vannuffel P; Zammattéo N; Remacle J

AUTHOR ADDRESS: (a)Laboratoire de Biochimie Cellulaire, Facultés Notre-Dame de la Paix, Rue de Bruxelles, 61, B-5000, Namur**Belgium E-Mail: sandrine.hamels@fundp.ac.be

JOURNAL: Biotechniques 31 (6):p1364-1372 December, 2001

MEDIUM: print

ISSN: 0736-6205

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: We propose the use of DNA microarray for the discrimination of homologous products after a single PCR amplification with consensus primers. The method was applied to **Staphylococcus** identification. The **femA** nucleotide-sequences, which are phylogenetically conserved among the **staphylococci**, were first amplified using a consensus primer pair together with the **mecA** sequence, a molecular marker for methicillin resistance. Products were then identified on a glass array. The microarray contained five selective DNA capture probes for the simultaneous and differential identification of the five most clinically relevant **staphylococcal** species (*S. aureus*, *S. epidermidis*, *S. haemolyticus*, *S. hominis*, and *S. saprophyticus*), while a consensus capture probe could detect all **femA** sequences, allowing the identification of the genus **Staphylococcus**. The **mecA** sequence hybridized to a specific capture probe. The identification was univocal because only a single capture probe had to be present for each sequence to be identified. The hybridization and identification processes were completed in less than 2 h. Current results demonstrate that low-density microarrays are powerful multigenotypic post-PCR analyzers and could compete with conventional bacteria identification.

5/7/2 (Item 2 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)

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12273661 BIOSIS NO.: 200000027163

Antibiotic resistance as a stress response: Complete sequencing of a large number of chromosomal loci in **Staphylococcus aureus** strain COL that impact on the expression of resistance to methicillin.

AUTHOR: de Lencastre H; Wu S W; Pinho M G; Ludovice A M; Filipe S; Gardete S; Sobral R; Gill S; Chung M; Tomasz A(a)

AUTHOR ADDRESS: (a)Rockefeller University, 1230 York Avenue, New York, NY, 10021**USA

JOURNAL: Microbial Drug Resistance 5 (3):p163-175 Fall, 1999

ISSN: 1076-6294

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

SUMMARY LANGUAGE: English

ABSTRACT: Tn551 inactivation has identified several determinants-fem or auxiliary genes-that, in addition to the **mecA** gene, are also critical for the expression of high-level and homogeneous resistance to methicillin. Genetic and/or biochemical analysis has shown that of the nearly dozen aux mutations described so far most are in genes involved in cell wall synthesis (**murE**, **pbp2**, **glmM**, **glnR**, **femA/B**, **llm**, etc.) or in complex regulatory functions (**sigmaB**), suggesting that optimal expression of resistance may involve the cooperative functioning of a number of genes in cell wall metabolism as well as stress response. The exact mechanism

of these functions is not known. In an attempt to explore this unusual aspect of methicillin resistance more fully, a Tn551 transposon library, constructed in the background of the highly and homogeneously methicillin-resistant **Staphylococcus aureus** strain COL, was screened for all independent insertional mutants in which the level of methicillin resistance of the parental strain (MIC, 1,600 mug/ml) was reduced by at least 15-fold and up to 500-fold. We now describe the sequencing of 21 Tn551-inactivated genes and their vicinities in 23 new auxiliary mutants that have been studied before. Using the inverted polymerase chain reaction (IPCR), we amplified fragments corresponding to the right and left junction of the Tn551 insertions, which were then sequenced by **primer** walking. The two largest groups of these new auxiliary genes encoded either proteins of unknown functions (6 genes) or showed homology with genes encoding proteins involved with putative sensory/regulatory activities (7 genes: protein kinases, ABC transporters, and a catabolite control protein). Sequencing upstream and downstream allowed the identification of a number of additional open reading frames, some of which may also include functions relevant for the expression of antibiotic resistance.

5/7/3 (Item 3 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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10975313 BIOSIS NO.: 199799596458
Investigation of a methicillin-resistant **Staphylococcus aureus** (MRSA) outbreak in an Irish hospital: Triplex PCR and DNA amplification fingerprinting.
AUTHOR: Cotter L; Lynch M; Cryan B; Greer P; Fanning S(a)
AUTHOR ADDRESS: (a)Medical Sci. Sect., Regional Technical Coll., Bishopstown, Cork**Ireland
JOURNAL: Journal of Hospital Infection 36 (1):p37-47 1997
ISSN: 0195-6701
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Methicillin-resistant **Staphylococcus aureus** (MRSA) is becoming a problematic nosocomial pathogen. A continuing increase in numbers of isolates is reported from Irish hospitals each year. Preventing cross-infection and the further spread of endemic strains requires effective control measures. This necessitates the development of sensitive methods for both detection and genetic identification of MRSA isolates. In this study, 48 MRSA strains isolated in the Cork University Hospital were analysed between January and July 1995 using a one-tube triplex-polymerase chain reaction (PCR), wherein three genes, the methicillin-resistance gene (*mecA*), *femA* and the extracellular thermonuclease gene, *nuc*, were simultaneously amplified. Methicillin-sensitive *S. aureus* (MSSA) and coagulase-negative **staphylococci** (CNS) were also tested and the assay was found to be MRSA specific. The genetic relationship among this collection of MRSA isolates was also investigated. A single **primer**, RW3A, derived from a well-characterized, repetitive sequence found in *Mycoplasma pneumoniae* produced discriminating DNA fragment arrays with all the study organisms. The patterns were reproducible, even after several passages of the isolates. Quantitative analysis of the patterns divided the collection into two main groups, DAF group I representing 48% of the collection and DAF group II a further 19%. The remaining strains showed unrelated patterns. To fully outline the distribution of MRSA in this area a larger study will be necessary. This paper outlines the applicability of both the identification and fingerprinting techniques to local strains.

5/7/4 (Item 4 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)
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10713234 BIOSIS NO.: 199799334379

Cloning and characterization of **femA** and femB from
Staphylococcus epidermidis.

AUTHOR: Alborn William E Jr; Hoskins Joann; Unal Serhat; Flokowitsch Jane E
; Hayes Carolyn A; Dotzlaf Joe E; Yeh W K; Skatrud Paul L(a)

AUTHOR ADDRESS: (a)Infectious Diseases Res., Eli Lilly and Co., Lilly Corp.
Cent., Indianapolis, IN 46285**USA

JOURNAL: Gene (Amsterdam) 180 (1-2):p177-181 1996

ISSN: 0378-1119

RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: A DNA fragment was identified and cloned from

Staphylococcus epidermidis (Se) using **femA** from *S. aureus*
(Sa) as a heterologous hybridization **probe**. DNA sequence analysis
of a portion of this clone revealed two complete ORFs highly related to
femA and femB of Sa. The genomic arrangement of the Se **femA/B**
complex was nearly identical to that observed in Sa. Intra- and
interspecies relatedness of these genes and conservation of genomic
organization were consistent with gene duplication of one of these genes
in an ancestral organism. Recombinant **FEMA**, produced in *Escherichia*
coli (Ec), was purified to near homogeneity. Identity of the purified
protein was verified by N-terminal amino acid (aa) sequence analysis.

5/7/5 (Item 5 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)
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08761984 BIOSIS NO.: 199395051335

Survey of the methicillin resistance-associated genes *mecA*, *mecR1-mecI*, and
femA-femB in clinical isolates of methicillin-resistant
Staphylococcus aureus.

AUTHOR: Hurlimann-Dalel Rocio L; Ryffel Cristina; Kayser Fritz H;
Berger-Bachi Brigitte(a)

AUTHOR ADDRESS: (a)Inst. Med. Microbiol., Univ. Zurich, Zurich**Switzerland

JOURNAL: Antimicrobial Agents and Chemotherapy 36 (12):p2617-2621 1992

ISSN: 0066-4804

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: The restriction site polymorphism of the chromosomal *femAB* region
and the first appearance of the regulatory element *mecR1-mecI* associated
with the methicillin resistance determinant (*mec*) were analyzed in 192
initially methicillin resistant (Mc-r) **Staphylococcus aureus**
clinical isolates collected between 1965 and 1990 in the Zurich area.
Forty-three of the strains lost the resistance spontaneously. All
isolates that were still Mc-r hybridized with *mecA*, the gene for the
low-affinity penicillin-binding protein PBP 2'. Mc-r strains isolated
before 1977 lacked sequences that hybridized when *mecR1-mecI*, a
regulatory element controlling the expression of *mecA*; exceptions to this
were one strain isolated in 1966 and one strain isolated in 1972. The
size of the *EcoRV* fragment carrying **femA**, a chromosomally encoded
factor involved in pentaglycine side chain formation of the peptidoglycan
and essential for the expression of methicillin resistance, was conserved
in all strains but one, which was susceptible to methicillin even though
it carried a functional *mecA* gene. The methicillin susceptibility of this
particular strain was presumably due to a spontaneous **femA**-like
mutation. The 192 strains belonged to seven different *EcoRV* restriction

577692

fragment patterns recognizable with a 10.5-kb **probe** covering the *femAB* region. Some 93% of the 149 Mc-r strains belonged to pattern A, and the remaining Mc-r strains shared patterns A' and B. The 42 isolates which spontaneously lost their resistance upon storage and revival represented all seven different patterns. This strong conservation of **femA** suggests an important role for **femA** in cell wall metabolism and methicillin resistance.

5/7/6 (Item 1 from file: 76)
DIALOG(R)File 76:Life Sciences Collection
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01648051 2864575

Survey of the methicillin resistance-associated genes *mecA*, *mecR1-mecI*, and **femA-femB** in clinical isolates of methicillin-resistant

Staphylococcus aureus.

Huerlimann Dalel, R.L.; Ryffel, C.; Kayser, F.H.; Berger Baechi, B.
Inst. Med. Microbiol., Univ. Zuerich, Zuerich, Switzerland
ANTIMICROB. AGENTS CHEMOTHER. vol. 36, no. 12, pp. 2617-2621 (1992.)
DOCUMENT TYPE: Journal article LANGUAGE: ENGLISH
SUBFILE: Microbiology Abstracts Section B: Bacteriology; Genetics Abstracts

The restriction site polymorphism of the chromosomal *femAB* region and the first appearance of the regulatory element *mecR1-mecI* associated with the methicillin resistance determinant (*mec*) were analyzed in 192 initially methicillin resistant (Mc super(r)) **Staphylococcus aureus** clinical isolates collected between 1965 and 1990 in the Zurich area. Forty-three of the strains lost the resistance spontaneously. All isolates that were still Mc super(r) hybridized with *mecA*, the gene for the low-affinity penicillin-binding protein PBP 2'. Mc super(r) strains isolated before 1977 lacked sequences that hybridized with *mecR1-mecI*, a regulatory element controlling the expression of *mecA* exceptions to this were one strain isolated in 1966 and one strain isolated in 1972. The size of the EcoRV fragment carrying **femA**, a chromosomally encoded factor involved in pentaglycine side chain formation of the peptidoglycan and essential for the expression of methicillin resistance, was conserved in all strains but one, which was susceptible to methicillin even though it carried a functional *mecA* gene. The methicillin susceptibility of this particular strain was presumably due to a spontaneous **femA**-like mutation. The 192 strains belonged to seven different EcoRV restriction fragment patterns recognizable with a 10.5-kb **probe** covering the *femAB* region. Some 93% of the 149 Mc super(r) strains belonged to pattern A, and the remaining Mc super(r) strains shared patterns A' and B. The 42 isolates which spontaneously lost their resistance upon storage and revival represented all seven different patterns. This strong conservation of **femA** suggests an important role for **femA** in cell wall metabolism and methicillin resistance.

5/7/7 (Item 1 from file: 94)
DIALOG(R)File 94:JICST-EPlus
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02362504 JICST ACCESSION NUMBER: 95A0390458 FILE SEGMENT: JICST-E
Molecular Epidemiology of **Staphylococcus** spp. Contamination in the

Ward Environment: Study on *mecA* and **femA** Genes in
Methicillin-Resistant Strains.

ASHIMOTO A (1); HAMADA T (1); ADACHI A (1); TANIGAWA T (1); TANAKA Y (1)
(1) Tottori Univ.

Kansenshogaku Zasshi(Journal of the Japanese Association for Infectious
Diseases), 1995, VOL.69,NO.1, PAGE.15-20, FIG.2, TBL.2, REF.13

JOURNAL NUMBER: Z0760AAY ISSN NO: 0387-5911

UNIVERSAL DECIMAL CLASSIFICATION: 613/614 579.22:616-022.1 616.9

LANGUAGE: English COUNTRY OF PUBLICATION: Japan
DOCUMENT TYPE: Journal
ARTICLE TYPE: Original paper
MEDIA TYPE: Printed Publication

ABSTRACT: **Staphylococcus** spp. were isolated from the ward environment and antibiotic susceptibility tests were performed. Twenty-nine strains out of 274 isolates were *S. aureus*, and 41.4% of the *S. aureus* strains were methicillin resistant (MRSA). All 12 strains of MRSA were also resistant to oxacillin, ceftizoxime, ampicillin and clindamycin. Among the coagulase-negative staphylococci (CNS), methicillin-resistant (MR) strains of *S. epidermidis*, *S. capitis*, *S. warneri*, *S. haemolyticus*, *S. hominis*, *S. auricularis*, *S. saprophyticus* and *S. cohnii* were isolated. Eight of the 10 *S. haemolyticus* strains were methicillin resistant. The **femA** gene was detected in *S. aureus* (MSSA and MRSA), but not in CNS by polymerase chain reaction (PCR) analysis and Southern blot analysis. The **mecA** gene was found in all the MRSA and MR-*S. epidermidis* strains tested, and one of the two MR-*S. hominis* strains, but not in MSSA, MS-*S. epidermidis*, MS-*S. hominis*, or MS-*S. haemolyticus*. DNA from one strain of MR-*S. hominis* and 2 strains of MR-*S. haemolyticus* was not amplified by PCR using the **mecA** gene primer, or hybridized by Southern blotting. The ambiguity that **mecA** was detected in some MR-CNS strains, but not in others is discussed. (author abstr.)

5/7/8 (Item 2 from file: 94)
DIALOG(R) File 94:JICST-Eplus
(c)2002 Japan Science and Tech Corp (JST). All rts. reserv.

02245000 JICST ACCESSION NUMBER: 94A0958267 FILE SEGMENT: JICST-E
Detection of Methicillin-Resistant **Staphylococcus aureus** Using PCR
and Non-Radioactive DNA Probes: III. Mutations of the **fem A**
Gene in Clinical Strains of **Staphylococcus aureus**.
YAMASHITA KEIKO (1); OTSUKA NORIMITSU (1); KAGAWA SHOHEI (1); MATSUOKA
AKIRA (1); TAKARADA YUTAKA (2); LI L (3)
(1) Hyogo Coll. of Med., Hosp.; (2) Toyobo Co., Ltd., Toyobo Res. Inst.
; (3) Chugokuidaidaiichibyoin
Rinsho Byori (Japanese Journal of Clinical Pathology), 1994, VOL.42, NO.10,
PAGE.1069-1076, FIG.2, TBL.3, REF.13

JOURNAL NUMBER: Z0687AAS ISSN NO: 0047-1860 CODEN: RBYOA
UNIVERSAL DECIMAL CLASSIFICATION: 579.22:577 575.2
LANGUAGE: Japanese COUNTRY OF PUBLICATION: Japan
DOCUMENT TYPE: Journal
ARTICLE TYPE: Original paper
MEDIA TYPE: Printed Publication

ABSTRACT: Methicillin resistance in *S. aureus* is primarily due to the presence of the **mec A** gene. However, in addition to **mec**, the phenotypic expression of methicillin resistance requires the presence of an additional gene (s), **fem A** which is chromosomally encoded. Previous studies suggest an increase in the biochemical function of **fem A** gene products due to base substitutions in the region upstream of the **fem A** gene and in its coding frame. The partial nucleotide sequences of **fem A** regions in reference and clinical strains of *S. aureus* were therefore analyzed by PCR-direct solid-phase sequencing and suitable DNA probes. Amplified target DNAs of 251, 330 and 271 bp were resolved on ethidium bromide stained gels and hybridized with DNA probes conjugated to alkaline phosphatase. In ATCC 12600 strain, a palindromic sequence was conserved in the region upstream of **fem A**. However, it was destroyed by the occurrence of mutations in other reference, and clinical strains tested regardless of whether they are methicillin-susceptible or resistant. Furthermore, in the coding frame of **fem A**, two missense mutations were present in MSSA and MRSA without any regularity. These findings suggest that mutations in the **fem A** region may not be a single factor essential for regulation of methicillin resistance, although **fem A** probably

functions cooperatively with mec A. (author abst.)

5/7/9 (Item 3 from file: 94)
DIALOG(R)File 94:JICST-EPlus
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01944598 JICST ACCESSION NUMBER: 93A0996304 FILE SEGMENT: JICST-E
MRSA. Detection of mecA and Its Regulatory Genes.
KAGAWA SHOHEI (1); YAMASHITA KEIKO (1); MATSUOKA AKIRA (1)
(1) Hyogo College of Medicine, Hospital
Rinsho Byori(Japanese Journal of Clinical Pathology), 1993, VOL.41,NO.11,
PAGE.1223-1231, FIG.3, TBL.3, REF.12
JOURNAL NUMBER: Z0687AAS ISSN NO: 0047-1860 CODEN: RBYOA
UNIVERSAL DECIMAL CLASSIFICATION: 616.9-07 579.222
LANGUAGE: Japanese COUNTRY OF PUBLICATION: Japan
DOCUMENT TYPE: Journal
ARTICLE TYPE: Original paper
MEDIA TYPE: Printed Publication

ABSTRACT: Methicillin resistance in *S. aureus* and *S. epidermidis* strains is primarily due to production of a new penicillin-binding protein PBP2' with extremely low binding affinity to most .BETA.-lactam antibiotics. The structural gene for PBP2', *mecA*, is detectable in clinical specimens by using the polymerase chain reaction(PCR). Amplified target DNA of 630bp can be resolved on ethidium bromide-stained gels, and hybridized with a **probe** conjugated to alkaline phosphatase. Survey for the *mecA* gene in 304 **staphylococci** revealed a good correlation between the presence of *mecA* and cultivation on agar plates with 4.MU.g/ml of oxacillin, although 3% of sensitive *S. aureus* strains had the *mecA* gene. On the other hand, analysis of the regulatory genes (orf 1 and 2) of methicillin resistance was performed on methicillin-resistant *S. aureus* strains N315 and MR108, demonstrating that the genome of MR108 lacks orf 2 which encodes the repressor protein (Hiramatsu et al., see Ref. 5). The regulatory genes of *mecA* were surveyed for 192 **staphylococci** by using PCR and allele-specific oligonucleotide probes: 76% of resistant *S. aureus* strains and 48% of resistant *S. epidermidis* strains possessed orf 1 corresponding to MR108 (constitutive-type strain), while the remainder of the resistant strains and two strains of sensitive *S. epidermidis* had two orfs of N315 (inducible-type strain). Furthermore, it appeared that mutation of the **femA** gene might not be an additional factor for expression of methicillin resistance. These observations suggest that *mecA* and its regulatory genes should be examined to understand how the genetic background contributed to the phenotypic expression of methicillin resistance in clinical strains. (author abst.)

5/7/10 (Item 4 from file: 94)
DIALOG(R)File 94:JICST-EPlus
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01910992 JICST ACCESSION NUMBER: 93A0899421 FILE SEGMENT: JICST-E
Detection of Methicillin-resistant **Staphylococcus aureus** Using PCR and Non-radioactive DNA Probes. (II).
MURAKI CHIKA (1); TAISHI KAORU (1); YAMASHITA KEIKO (1); OTSUKA NORIMITSU (1); KAGAWA SHOHEI (1); MATSUOKA AKIRA (1)
(1) Hyogo College of Medicine, Hospital
Rinsho Byori(Japanese Journal of Clinical Pathology), 1993, VOL.41,NO.10,
PAGE.1159-1166, FIG.3, TBL.3, REF.8
JOURNAL NUMBER: Z0687AAS ISSN NO: 0047-1860 CODEN: RBYOA
UNIVERSAL DECIMAL CLASSIFICATION: 616-078
LANGUAGE: Japanese COUNTRY OF PUBLICATION: Japan
DOCUMENT TYPE: Journal
ARTICLE TYPE: Original paper

MEDIA TYPE: Printed Publication

ABSTRACT: Methicillin resistance in **staphylococci** is primarily due to the presence of a *mec A* gene which encodes the novel penicillin-binding protein 2'. Some chromosomal factors, **fem A** and *fem B*, also participate in the expression of methicillin resistance in *S. aureus*. This study was designed to detect *mec A*, **fem A** and *fem B* genes for identification of **staphylococcal** species and for discrimination of methicillin-resistant cells. Three different pairs of DNA primers (PBP2' AF-PBP2' AR, *fem* AF-*fem* AR and *fem* BF-*fem* BR) complementary to unique regions of *mec A*, **fem A** and *fem B* genes were synthesized for use in polymerase chain reaction with DNAs of methicillin-sensitive *S. aureus*(MSSA), *S. epidermidis*, methicillin-resistant *S. aureus*(MRSA) and *S. epidermidis*. Amplified target DNAs of 630, 509, and 651 bp were resolved on ethidium bromide-stained gel, and hybridized to DNA probes conjugated to alkaline phosphatase. When applied to pure cultures on the MRSA screen agar, all three DNA probes tested detected MRSA in 47 of 61 culture-positive specimens (77.1%); the detection ratio of MRSA with *mec A* and either **fem A** or *fem B* probes was increased to 95.9%. By contrast, the **fem A** and *fem B* probes did not detect *S. epidermidis*. The result of detecting these species streaked on mannitol-salt agar were similar, while the detection of MSSA with the **fem A** and *fem B* probes was incomplete irrespective of the presence or absence of *mec A*. These findings suggest a good correlation between cultivation and DNA **probe** assay with respect to MRSA detection. (author abst.)

5/7/11 (Item 1 from file: 399)

DIALOG(R)File 399:CA SEARCH(R)

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130279197 CA: 130(21)279197r PATENT

Typing of strains of *Staphylococcus* using variation in the *femA* gene

INVENTOR(AUTHOR): Vannuffel, Pascal; Gala, Jean-Luc

LOCATION: Belg.

ASSIGNEE: Universite Catholique de Louvain; Ministere de la Defense

Nationale

PATENT: PCT International ; WO 9916780 A2 DATE: 19990408

APPLICATION: WO 98BE141 (19980928)

PAGES: 48 pp. CODEN: PIXXD2 LANGUAGE: English CLASS: C07H-021/00A

DESIGNATED COUNTRIES: CA; JP; US DESIGNATED REGIONAL: AT; BE; CH; CY; DE ; DK; ES; FI; FR; GB; GR; IE; IT; LU; MC; NL; PT; SE

SECTION:

CA210001 MICROBIAL, ALGAL, AND FUNGAL BIOCHEMISTRY

CA203XXX Biochemical Genetics

CA209XXX Biochemical Methods

CA214XXX Mammalian Pathological Biochemistry

IDENTIFIERS: *Staphylococcus* typing *femA* gene consensus variation

DESCRIPTORS:

Polymorphism(genetic)...

at *femA* gene, in typing of *Staphylococcus*; typing of strains of

Staphylococcus using variation in *femA* gene

Staphylococcus capitis... *Staphylococcus cohnii*... *Staphylococcus*

gallinarum... *Staphylococcus hemolyticus*... *Staphylococcus hominis*...

Staphylococcus lugdunensis... *Staphylococcus saprophyticus*...

Staphylococcus schleiferi... *Staphylococcus sciuri*... *Staphylococcus*

simulans... *Staphylococcus warneri*... *Staphylococcus xylosus*...

femA gene of; typing of strains of *Staphylococcus* using variation in

femA gene

Genes(microbial)...

femA; typing of strains of *Staphylococcus* using variation in *femA* gene

Primers(nucleic acid)... Probes(nucleic acid)...

for *femA* gene, in typing of *Staphylococcus*; typing of strains of

Staphylococcus using variation in femA gene
Nucleic acid hybridization...
for typing of Staphylococcus; typing of strains of Staphylococcus using
variation in femA gene
Genes(microbial)...
mecA, in typing of Staphylococcus; typing of strains of Staphylococcus
using variation in femA gene
PCR(polymerase chain reaction)...
multiplex, of femA and mecA genes, in typing of Staphylococcus; typing
of strains of Staphylococcus using variation in femA gene
Protein sequences...
of femA gene products of Staphylococcus spp.; typing of strains of
Staphylococcus using variation in femA gene
DNA sequences...
of femA genes of Staphylococcus spp.; typing of strains of
Staphylococcus using variation in femA gene
Molecular diagnosis...
of Staphylococcus infection; typing of strains of Staphylococcus using
variation in femA gene
Staphylococcus...
typing of strains of Staphylococcus using variation in femA gene
CAS REGISTRY NUMBERS:
222617-88-1 222617-89-2 222617-91-6 222617-94-9 222617-97-2
222617-99-4 222716-95-2 222716-99-6 amino acid sequence; typing of
strains of Staphylococcus using variation in femA gene
222617-90-5 222617-93-8 222617-95-0 222617-98-3 222618-00-0
222716-93-0 222716-94-1 222716-98-5 nucleotide sequence; typing of
strains of Staphylococcus using variation in femA gene
222617-77-8 222617-78-9 222617-79-0 222617-81-4 222617-82-5
222617-83-6 222617-84-7 222617-86-9 222617-87-0 222618-01-1
222618-02-2 222618-03-3 222618-04-4 222618-05-5 222618-06-6
222618-07-7 222618-08-8 222618-09-9 222618-10-2 222618-11-3
222618-12-4 222618-13-5 222618-14-6 primer for amplification of femA
gene in typing of Staphylococcus; typing of strains of Staphylococcus
using variation in femA gene

5/7/12 (Item 2 from file: 399)
DIALOG(R)File 399:CA SEARCH(R)
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129255617 CA: 129(20)255617f JOURNAL
Rapid and specific molecular identification of methicillin-resistant
Staphylococcus aureus in endotracheal aspirates from mechanically
ventilated patients
AUTHOR(S): Vannuffel, Pascal; Laterre, Pierre-Francois; Bouyer, Michele;
Gigi, Jacques; Vandercam, Bernard; Reynaert, Marc; Gala, Jean-Luc
LOCATION: Laboratory of Applied Molecular Technology, St. Luc University
Hospital, B-1200, Brussels, Belg.
JOURNAL: J. Clin. Microbiol. DATE: 1998 VOLUME: 36 NUMBER: 8 PAGES:
2366-2368 CODEN: JCMIDW ISSN: 0095-1137 LANGUAGE: English PUBLISHER:
American Society for Microbiology
SECTION:
CA203001 Biochemical Genetics
CA210XXX MICROBIAL, ALGAL, AND FUNGAL BIOCHEMISTRY
CA214XXX Mammalian Pathological Biochemistry
IDENTIFIERS: methicillin resistance Staphylococcus diagnosis PCR primers
DESCRIPTORS:
Genes(microbial)...
femA; rapid and specific mol. identification of methicillin-resistant
Staphylococcus aureus in endotracheal aspirates from mech. ventilated
patients
Genes(microbial)...
mecA; rapid and specific mol. identification of methicillin-resistant

Staphylococcus aureus in endotracheal aspirates from mech. ventilated patients
 Staphylococcus aureus...
 methicillin-resistant; rapid and specific mol. identification of
 methicillin-resistant Staphylococcus aureus in endotracheal aspirates
 from mech. ventilated patients
 Molecular diagnosis... PCR(polymerase chain reaction)...
 rapid and specific mol. identification of methicillin-resistant
 Staphylococcus aureus in endotracheal aspirates from mech. ventilated
 patients
 Antibiotic resistance...
 to methicillin; rapid and specific mol. identification of
 methicillin-resistant Staphylococcus aureus in endotracheal aspirates
 from mech. ventilated patients
 CAS REGISTRY NUMBERS:
 171174-37-1 171174-38-2 PCR primer, for femA; rapid and specific mol.
 identification of methicillin-resistant Staphylococcus aureus in
 endotracheal aspirates from mech. ventilated patients
 171174-35-9 171174-36-0 PCR primer, for mecA; rapid and specific mol.
 identification of methicillin-resistant Staphylococcus aureus in
 endotracheal aspirates from mech. ventilated patients

5/7/13 (Item 3 from file: 399)
 DIALOG(R)File 399:CA SEARCH(R)
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124001787 CA: 124(1)1787c JOURNAL
 Specific detection of methicillin-resistant Staphylococcus species by
 multiplex PCR
 AUTHOR(S): Vannuffel, Pascal; Gigi, Jacques; Ezzedine, Houda; Vandercam,
 Bernard; Delmee, Michel; Wauters, Georges; Gala, Jean-Luc
 LOCATION: St. Luc University Hospital, B-1200, Brussels, Belg.
 JOURNAL: J. Clin. Microbiol. DATE: 1995 VOLUME: 33 NUMBER: 11 PAGES:
 2864-7 CODEN: JCMIDW ISSN: 0095-1137 LANGUAGE: English
 SECTION:
 CA203001 Biochemical Genetics
 CA210XXX MICROBIAL, ALGAL, AND FUNGAL BIOCHEMISTRY
 IDENTIFIERS: methicillin resistance PCR Staphylococcus
 DESCRIPTORS:
 Polymerase chain reaction...
 multiplex; specific detection of methicillin-resistant Staphylococcus
 species by multiplex PCR
 Gene,microbial, femA... Gene,microbial, mecA... Staphylococcus...
 specific detection of methicillin-resistant Staphylococcus species by
 multiplex PCR
 CAS REGISTRY NUMBERS:
 171174-35-9 171174-36-0 171174-37-1 171174-38-2 171174-39-3
 171174-40-6 171174-41-7 primer; specific detection of
 methicillin-resistant Staphylococcus species by multiplex PCR
 61-32-5 resistance; specific detection of methicillin-resistant
 Staphylococcus species by multiplex PCR

5/7/14 (Item 4 from file: 399)
 DIALOG(R)File 399:CA SEARCH(R)
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119196746 CA: 119(19)196746r JOURNAL
 Detection of methicillin-resistant Staphylococcus aureus by in vitro
 enzymatic amplification of mecA and femA genes
 AUTHOR(S): Oshima, Toshio; Miyachi, Hayato; Fusegawa, Hisae; Masukawa,
 Atsuko; Ikeda, Masakatsu; Ando, Yasuhiko
 LOCATION: Hosp., Tokai Univ., Isehara, Japan, 259-11

JOURNAL: Rinsho Byori DATE: 1993 VOLUME: 41 NUMBER: 7 PAGES: 773-8
CODEN: RBYOAI ISSN: 0047-1860 LANGUAGE: Japanese

SECTION:

CA203001 Biochemical Genetics

CA210XXX Microbial Biochemistry

IDENTIFIERS: methicillin resistance Staphylococcus detection gene PCR,
mecA femA gene Staphylococcus detection PCR

DESCRIPTORS:

Polymerase chain reaction...

for methicillin-resistant Staphylococcus aureus detection, mecA and
femA genes amplification in

Staphylococcus aureus...

methicillin-resistant, PCR detection of, mecA and femA genes
amplification in

Gene,microbial, femA... Gene,microbial, mecA...

PCR amplification of, for detection of methicillin-resistant
Staphylococcus aureus

CAS REGISTRY NUMBERS:

150742-28-2 150742-29-3 150742-31-7 150742-32-8 PCR primer, for
methicillin-resistant Staphylococcus aureus detection

150742-30-6 150742-33-9 PCR probe, for methicillin-resistant
Staphylococcus aureus detection

61-32-5 Staphylococcus aureus resistance to, detection of, mecA and femA
genes amplification by PCR in

5/7/15 (Item 5 from file: 399)

DIALOG(R)File 399:CA SEARCH(R)

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118033633 CA: 118(5)33633s JOURNAL

Detection of methicillin-resistant staphylococci by using the polymerase
chain reaction

AUTHOR(S): Unal, Serhat; Hoskins, Joann; Flokowitsch, Jane E.; Wu, C. Y.
Ernie; Preston, David A.; Skatrud, Paul L.

LOCATION: Eli Lilly and Co., Indianapolis, IN, 46285, USA

JOURNAL: J. Clin. Microbiol. DATE: 1992 VOLUME: 30 NUMBER: 7 PAGES:
1685-91 CODEN: JCMIDW ISSN: 0095-1137 LANGUAGE: English

SECTION:

CA203001 Biochemical Genetics

CA210XXX Microbial Biochemistry

IDENTIFIERS: Staphylococcus methicillin resistance gene detection PCR

DESCRIPTORS:

Polymerase chain reaction...

for detection of methicillin resistance genes, in Staphylococcus

Gene,microbial, femA... Gene,microbial, mecA...

for methicillin resistance, polymerase chain reaction detection of, in
Staphylococcus

Proteins,specific or class, PBP 2A (penicillin-binding protein 2A)...

methicillin resistance gene mecA for, polymerase chain reaction
detection of, in Staphylococcus

Staphylococcus aureus... Staphylococcus epidermidis... Staphylococcus

hemolyticus... Staphylococcus simulans...

methicillin resistance genes of, polymerase chain reaction for
detection of

Antibiotic resistance...

to methicillin, genes for, polymerase chain reaction detection of, in
Staphylococcus

CAS REGISTRY NUMBERS:

143349-63-7 143349-74-0 143349-81-9 143369-87-3 143374-79-2

145187-83-3 as DNA primer, in polymerase chain reaction detection of
methicillin resistance gene in Staphylococcus

9001-13-2 of Staphylococcus, PCR detection of methicillin resistance gene
in relation to

61-32-5 resistance to, genes for, polymerase chain reaction detection of,
in Staphylococcus
?

WEST[Generate Collection](#)[Print](#)**Search Results - Record(s) 21 through 26 of 26 returned.**☐ 21. Document ID: WO 9916780 A2

L4: Entry 21 of 26

File: EPAB

Apr 8, 1999

PUB-NO: WO009916780A2

DOCUMENT-IDENTIFIER: WO 9916780 A2

TITLE: GENETIC SEQUENCES, DIAGNOSTIC AND/OR QUANTIFICATION METHODS AND DEVICES FOR THE IDENTIFICATION OF STAPHYLOCOCCI STRAINS

PUBN-DATE: April 8, 1999

INVENTOR-INFORMATION:

NAME

COUNTRY

VANNUFFEL, PASCAL

BE

GALA, JEAN-LUC

BE

INT-CL (IPC): C07 H 21/00

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	KWIC
Draw	Desc	Image									

☐ 22. Document ID: US 5587307 A

L4: Entry 22 of 26

File: EPAB

Dec 24, 1996

PUB-NO: US005587307A

DOCUMENT-IDENTIFIER: US 5587307 A

TITLE: FemA gene of staphylococcus epidermidis, femA protein, and vectors and microorganisms comprising the femA gene

PUBN-DATE: December 24, 1996

INVENTOR-INFORMATION:

NAME

COUNTRY

ALBORN, JR WILLIAM E

US

HOSKINS, JOANN

US

SKATRUD, PAUL L

US

UENAL, SERHAT

TR

INT-CL (IPC): C12 N 15/31; C12 N 15/70; C07 K 14/31

EUR-CL (EPC): C07K014/31

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	KWIC
Draw	Desc	Image									

☐ 23. Document ID: EP 625575 A2

L4: Entry 23 of 26

File: EPAB

Nov 23, 1994

PUB-NO: EP000625575A2

DOCUMENT-IDENTIFIER: EP 625575 A2

TITLE: Fem A gene of staphylococcus epidermidis, fem A protein, and vectors of microorganisms comprising the fem A gene.

PUBN-DATE: November 23, 1994

INVENTOR-INFORMATION:

NAME	COUNTRY
ALBORN, WILLIAM ERNEST JR	US
HOSKINS, JO ANN	US
SKATRUD, PAUL LUTHER	US
UENAL, SERHAT	TR

INT-CL (IPC): C12N 15/31; C12P 21/02; C07K 13/00

EUR-CL (EPC): C07K014/31

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	WWW
Draw Desc	Image									

☐ 24. Document ID: AU 200111210 A, EP 1096024 A1, WO 200131055 A2

L4: Entry 24 of 26

File: DWPI

May 8, 2001

DERWENT-ACC-NO: 2001-309857

DERWENT-WEEK: 200149

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TITLE: Detecting, quantifying multiple target nucleotide sequences in biological sample for detecting microorganisms or genetic characteristics, by amplifying target sequence and hybridizing on single stranded capture probes

INVENTOR: ALEXANDRE, I; DE LONGUEVILLE, F ; HAMELS, S ; REMACLE, J ; ZAMMATTEO, N

PRIORITY-DATA: 1999EP-0870226 (October 28, 1999)

PATENT-FAMILY:

PUB-NO	PUB-DATE	LANGUAGE	PAGES	MAIN-IPC
AU 200111210 A	May 8, 2001		000	C12Q001/68
EP 1096024 A1	May 2, 2001	E	027	C12Q001/68
WO 200131055 A2	May 3, 2001	E	000	C12Q001/68

INT-CL (IPC): C12 Q 1/68

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	WWW
Draw Desc	Image									

☐ 25. Document ID: JP 2001518283 W, WO 9916780 A2, EP 1017850 A2

L4: Entry 25 of 26

File: DWPI

Oct 16, 2001

DERWENT-ACC-NO: 1999-287521

DERWENT-WEEK: 200176

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TITLE: New Staphylococcus-specific oligonucleotides

INVENTOR: GALA, J; VANNUFFEL, P

PRIORITY-DATA: 1997EP-0870146 (September 26, 1997)

PATENT-FAMILY:

PUB-NO	PUB-DATE	LANGUAGE	PAGES	MAIN-IPC
JP 2001518283 W	October 16, 2001		057	C12Q001/68
WO 9916780 A2	April 8, 1999	E	047	C07H021/00
EP 1017850 A2	July 12, 2000	E	000	C12Q001/68

INT-CL (IPC): C07 H 21/00; C12 N 15/09; C12 N 15/31; C12 Q 1/68

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments
Draw Desc	Image								

KWC

☐ 26. Document ID: US 5587307 A, EP 625575 A2, AU 9461802 A, CA 2122202 A, JP 06319561 A, EP 625575 A3, HU 70300 T

L4: Entry 26 of 26

File: DWPI

Dec 24, 1996

DERWENT-ACC-NO: 1994-359748

DERWENT-WEEK: 199706

COPYRIGHT 2002 DERWENT INFORMATION LTD

TITLE: Isolated femA gene of Staphylococcus epidermidis - used to develop agents for inhibiting FemA protein for use in treating methicillin-resista nt bacteria

INVENTOR: ALBORN, W E; HOSKINS, J A ; SKATRUD, P L ; UNAL, S ; UENAL, S ; HOSKINS, J

PRIORITY-DATA: 1993US-0057163 (April 30, 1993), 1994US-0208925 (March 9, 1994), 1994US-0330154 (October 27, 1994)

PATENT-FAMILY:

PUB-NO	PUB-DATE	LANGUAGE	PAGES	MAIN-IPC
US 5587307 A	December 24, 1996		014	C12N015/31
EP 625575 A2	November 23, 1994	E	023	C12N015/31
AU 9461802 A	November 3, 1994		000	C12N015/31
CA 2122202 A	October 31, 1994		000	C12N015/31
JP 06319561 A	November 22, 1994		023	C12N015/31
EP 625575 A3	February 22, 1995		000	C12N015/31
HU 70300 T	September 28, 1995		000	C12N009/00

INT-CL (IPC): C07K 13/00; C07K 14/31; C12N 1/21; C12N 9/00; C12N 15/31; C12N 15/32; C12N 15/52; C12N 15/66; C12N 15/70; C12N 15/74; C12P 21/02; C12N 15/31; C12R 1/44; C12N 1/21; C12R 1/19; C12P 21/02; C12R 1/19

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments
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KWC

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Terms	Documents
L3 and femA	26

Display Format:

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L4: Entry 1 of 26

File: PGPB

Jun 13, 2002

PGPUB-DOCUMENT-NUMBER: 20020072105

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20020072105 A1

TITLE: Crystallization and structure determination of FemA and FemA-like proteins

PUBLICATION-DATE: June 13, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Benson, Timothy E.	Kalamazoo	MI	US	
Prince, Donald Bryan	Parchment	MI	US	

US-CL-CURRENT: 435/219; 702/19

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments
Draw	Desc	Image							

[RMC](#)☐ 2. Document ID: US 6403337 B1

L4: Entry 2 of 26

File: USPT

Jun 11, 2002

US-PAT-NO: 6403337

DOCUMENT-IDENTIFIER: US 6403337 B1

TITLE: Staphylococcus aureus genes and polypeptides

DATE-ISSUED: June 11, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Bailey; Camella	Washington	DC		
Choi; Gil H.	Rockville	MD		

US-CL-CURRENT: 435/69.7; 435/252.3, 435/320.1, 435/468, 536/23.7

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments
Draw	Desc	Image							

[RMC](#)☐ 3. Document ID: US 6391614 B1

L4: Entry 3 of 26

File: USPT

May 21, 2002

US-PAT-NO: 6391614

DOCUMENT-IDENTIFIER: US 6391614 B1

TITLE: Auxiliary gene and protein of methicillin resistant bacteria and antagonists thereof

DATE-ISSUED: May 21, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Tomasz; Alexander	New York	NY		
De Lencastre; Herminia	New York	NY		

US-CL-CURRENT: 435/253.2; 435/320.1, 536/23.1

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments
Draw	Desc	Image							

RMC

☐ 4. Document ID: US 6376180 B1

L4: Entry 4 of 26

File: USPT

Apr 23, 2002

US-PAT-NO: 6376180

DOCUMENT-IDENTIFIER: US 6376180 B1

TITLE: Methods of identifying compounds that bind to target species under isothermal denaturing conditions

DATE-ISSUED: April 23, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Tomich; Paul K.	Kalamazoo	MI		
Epps; Dennis E.	Portage	MI		
Kezdy; Ferenc J.	Kalamazoo	MI		
Marschke; Charles K.	Kalamazoo	MI		
Sarver; Ronald W.	Paw Paw	MI		

US-CL-CURRENT: 435/6; 435/4, 435/7.1, 436/172, 436/518, 436/805

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments
Draw	Desc	Image							

RMC

☐ 5. Document ID: US 6356845 B1

L4: Entry 5 of 26

File: USPT

Mar 12, 2002

US-PAT-NO: 6356845

DOCUMENT-IDENTIFIER: US 6356845 B1

TITLE: Crystallization and structure determination of Staphylococcus aureus UDP-N-acetylenolpyruvylglucosamine reductase (S. aureus MurB)

DATE-ISSUED: March 12, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Benson; Timothy E.	Kalamazoo	MI		
Harris; Melissa S.	Marshall	MI		

US-CL-CURRENT: 702/19; 435/183, 702/27

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	KWIC
Draw Desc	Image									

☐ 6. Document ID: US 6297273 B1

L4: Entry 6 of 26

File: USPT

Oct 2, 2001

US-PAT-NO: 6297273

DOCUMENT-IDENTIFIER: US 6297273 B1

TITLE: Use of cocoa solids having high cocoa polyphenol content in tableting compositions and capsule filling compositions

DATE-ISSUED: October 2, 2001

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Romanczyk, Jr.; Leo J.	Hackettstown	NJ		

US-CL-CURRENT: 514/456; 424/452, 424/465, 426/631, 549/399, 549/407

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	KWIC
Draw Desc	Image									

☐ 7. Document ID: US 6251647 B1

L4: Entry 7 of 26

File: USPT

Jun 26, 2001

US-PAT-NO: 6251647

DOCUMENT-IDENTIFIER: US 6251647 B1

TITLE: Auxiliary genes and proteins of methicillin resistant bacteria and antagonists thereof

DATE-ISSUED: June 26, 2001

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
de Lencastre; Herminia	New York	NY		
Tomasz; Alexander	New York	NY		

US-CL-CURRENT: 435/193; 435/252.1, 435/252.33, 435/320.1, 435/471, 536/23.1

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	KWIC
Draw Desc	Image									

☐ 8. Document ID: US 6228588 B1

L4: Entry 8 of 26

File: USPT

May 8, 2001

US-PAT-NO: 6228588

DOCUMENT-IDENTIFIER: US 6228588 B1

TITLE: Methods of screening for compounds active on Staphylococcus aureus target genes

DATE-ISSUED: May 8, 2001

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Benton; Bret	Burlingame	CA		
Lee; Ving J.	Los Altos	CA		
Malouin; Francois	Los Gatos	CA		
Martin; Patrick K.	Sunnyvale	CA		
Schmid; Molly B.	Menlo Park	CA		
Sun; Dongxu	Cupertino	CA		

US-CL-CURRENT: 435/6; 435/69.1, 514/2, 514/44

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments
Draw Desc	Image								

KMC

☐ 9. Document ID: US 6187541 B1

L4: Entry 9 of 26

File: USPT

Feb 13, 2001

US-PAT-NO: 6187541

DOCUMENT-IDENTIFIER: US 6187541 B1

TITLE: Methods of screening for compounds active on staphylococcus aureus target genes

DATE-ISSUED: February 13, 2001

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Benton; Bret	Burlingame	CA		
Lee; Ving J.	Los Altos	CA		
Malouin; Francois	Los Gatos	CA		
Martin; Patrick K.	Sunnyvale	CA		
Schmid; Molly B.	Menlo Park	CA		
Sun; Dongxu	Cupertino	CA		

US-CL-CURRENT: 435/6; 435/69.1, 514/2, 514/44

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments
Draw Desc	Image								

KMC

☐ 10. Document ID: US 6136587 A

L4: Entry 10 of 26

File: USPT

Oct 24, 2000

US-PAT-NO: 6136587

DOCUMENT-IDENTIFIER: US 6136587 A

TITLE: Auxiliary genes and proteins of methicillin resistant bacteria and antagonists thereof

DATE-ISSUED: October 24, 2000

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Tomasz; Alexander	New York	NY		
De Lencastre; Herminia	New York	NY		

US-CL-CURRENT: 435/252.3; 435/253.4, 435/320.1, 536/23.1, 536/23.7

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments
Draw Desc	Image								

KMC

☐ 11. Document ID: US 6077513 A

L4: Entry 11 of 26

File: USPT

Jun 20, 2000

US-PAT-NO: 6077513

DOCUMENT-IDENTIFIER: US 6077513 A

TITLE: Drug for treatment of bilharziasis (Schistosomiasis)

DATE-ISSUED: June 20, 2000

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Massoud; Ahmed Mohamed Ali	Cairo			EGX

US-CL-CURRENT: 424/748; 424/405, 424/439, 424/456, 426/651

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments
Draw Desc	Image								

KMC

☐ 12. Document ID: US 6063613 A

L4: Entry 12 of 26

File: USPT

May 16, 2000

US-PAT-NO: 6063613

DOCUMENT-IDENTIFIER: US 6063613 A

TITLE: Auxiliary genes and proteins of methicillin resistant bacteria and antagonists thereof

DATE-ISSUED: May 16, 2000

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
De Lencastre; Herminia	New York	NY		
Tomasz; Alexander	New York	NY		

US-CL-CURRENT: 435/252.3; 435/32

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	RWC
Draw Desc	Image									

☐ 13. Document ID: US 6037123 A

L4: Entry 13 of 26

File: USPT

Mar 14, 2000

US-PAT-NO: 6037123

DOCUMENT-IDENTIFIER: US 6037123 A

TITLE: Methods of screening for compounds active on Staphylococcus aureus target genes

DATE-ISSUED: March 14, 2000

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Benton; Bret	Burlingame	CA		
Lee; Ving J.	Los Altos	CA		
Malouin; Francois	Los Gatos	CA		
Martin; Patrick K.	Sunnyvale	CA		
Schmid; Molly B.	Menlo Park	CA		
Sun; Dongxu	Cupertino	CA		

US-CL-CURRENT: 435/6; 435/69.1, 436/501, 514/2, 514/44

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	RWC
Draw Desc	Image									

☐ 14. Document ID: US 6013507 A

L4: Entry 14 of 26

File: USPT

Jan 11, 2000

US-PAT-NO: 6013507

DOCUMENT-IDENTIFIER: US 6013507 A

TITLE: Auxiliary genes and proteins of methicillin resistant bacteria and antagonists thereof

DATE-ISSUED: January 11, 2000

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Tomasz; Alexander	New York	NY		
De Lencastre; Herminia	New York	NY		

US-CL-CURRENT: 435/252.3; 435/252.1, 435/320.1, 536/23.7

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	RWC
Draw Desc	Image									

☐ 15. Document ID: US 5985643 A

L4: Entry 15 of 26

File: USPT

Nov 16, 1999

US-PAT-NO: 5985643

DOCUMENT-IDENTIFIER: US 5985643 A

TITLE: Auxiliary gene and protein of methicillin resistant bacteria and antagonists thereof

DATE-ISSUED: November 16, 1999

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Tomasz; Alexander	New York	NY		
De Lencastre; Herminia	New York	NY		

US-CL-CURRENT: 435/243; 435/883, 536/23.7

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	KMC
Draw	Desc	Image								

☐ 16. Document ID: US 5883074 A

L4: Entry 16 of 26

File: USPT

Mar 16, 1999

US-PAT-NO: 5883074

DOCUMENT-IDENTIFIER: US 5883074 A

TITLE: Potentiators of antibacterial agents

DATE-ISSUED: March 16, 1999

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Boggs; Amy	Menlo Park	CA		
Trias; Joaquim	San Mateo	CA		
Hecker; Scott	Los Gatos	CA		

US-CL-CURRENT: 514/8; 514/11, 514/152, 514/153, 514/154, 514/197, 514/198, 514/199, 514/29, 514/312, 514/37, 514/39

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	KMC
Draw	Desc	Image								

☐ 17. Document ID: US 5776712 A

L4: Entry 17 of 26

File: USPT

Jul 7, 1998

US-PAT-NO: 5776712

DOCUMENT-IDENTIFIER: US 5776712 A

TITLE: Methods and materials for the detection of Staphylococcus aureus

DATE-ISSUED: July 7, 1998

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Kuusela; Pentti	Helsinki			FIN
Hilden; Pekka	Helsinki			FIN

US-CL-CURRENT: 435/7.33; 424/243.1, 435/7.32, 436/547, 530/387.1, 530/388.4,
530/389.5

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	KMC
Draw Desc	Image									

☐ 18. Document ID: US 5661104 A

L4: Entry 18 of 26

File: USPT

Aug 26, 1997

US-PAT-NO: 5661104

DOCUMENT-IDENTIFIER: US 5661104 A

TITLE: Preservative compositions for use in aqueous systems

DATE-ISSUED: August 26, 1997

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Virgilio; Joseph A.	Wayne	NJ		

US-CL-CURRENT: 504/150; 514/741

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	KMC
Draw Desc	Image									

☐ 19. Document ID: US 5587307 A

L4: Entry 19 of 26

File: USPT

Dec 24, 1996

US-PAT-NO: 5587307

DOCUMENT-IDENTIFIER: US 5587307 A

TITLE: FemA gene of staphylococcus epidermidis, femA protein, and vectors and microorganisms comprising the femA gene

DATE-ISSUED: December 24, 1996

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Alborn, Jr.; William E.	Carmel	IN		
Hoskins; JoAnn	Indianapolis	IN		
Skatrud; Paul L.	Greenwood	IN		
Unal; Serhat	Ankara			TRX

US-CL-CURRENT: 435/325; 435/252.3, 435/252.33, 530/350, 536/23.7

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	KMC
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☐ 20. Document ID: JP 06319561 A

L4: Entry 20 of 26

File: JPAB

Nov 22, 1994

WEST Search History

DATE: Wednesday, June 26, 2002

<u>Set Name</u> side by side	<u>Query</u>	<u>Hit Count</u>	<u>Set Name</u> result set
<i>DB=USPT,PGPB,JPAB,EPAB,DWPI; PLUR=YES; OP=ADJ</i>			
L5	L3 and (fem adj A)	0	L5
L4	L3 and femA	26	L4
L3	staphylococc\$	22698	L3
L2	L1	15228	L2
<i>DB=USPT; PLUR=YES; OP=ADJ</i>			
L1	staphylococc\$	15228	L1

END OF SEARCH HISTORY

SYSTEM:OS - DIALOG OneSearch

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File 6:NTIS 1964-2002/Jul W1
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See HELP NEWS 305.

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Set	Items	Description
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? s staphylococc\$		
S1	0	STAPHYLOCOCC\$
? s staphylococc?		
S2	406639	STAPHYLOCOCC?
? s s2 and (femA or fem (w) A)		
Processing		
Processing		
Processing		
Processed	10 of 25 files ...	
Processing		
Processing		
Processed	20 of 25 files ...	
Processing		
Completed processing all files		
	406639	S2
	1453	FEMA
	31810	FEM
	53740838	A
	318	FEM(W)A
S3	378	S2 AND (FEMA OR FEM (W) A)
? s s3 and (probe or primer)		
	378	S3
	666311	PROBE
	149805	PRIMER
S4	42	S3 AND (PROBE OR PRIMER)
? rd s4		
...completed examining records		
S5	15	RD S4 (unique items)
? t s5/7/1-15		

PUB-NO: JP406319561A

DOCUMENT-IDENTIFIER: JP 06319561 A

TITLE: FEMA GENE OF STAPHYLOCOCCUS EPIDERMIDIS, FEMA PROTEIN, AND VECTOR AND MICROORGANISM COMPRISING THE FEMA GENE

PUBN-DATE: November 22, 1994

INVENTOR-INFORMATION:

NAME

COUNTRY

ALBORN, JR WILLIAM ERNEST

HOSKINS, JO ANN

SKATRUD, PAUL LUTHER

UENAL, SERHAT

INT-CL (IPC): C12N 15/31; C12N 1/21; C12P 21/02

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